

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 1999, 10:11:21 ; Search time 6413.31 Seconds

(without alignments)  
3185.777 Million cell updates/sec

Title: US-08-798-691A-3

Perfect score: 5711

Sequence: 1 AGCTGCGTGAAGACTTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 1788773984 residues

Database: GenEmbl:\*

- 1: gb\_bal:\*
- 2: gb\_ba2:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_p11:\*
- 9: gb\_p12:\*
- 10: gb\_p1:\*
- 11: gb\_p12:\*
- 12: gb\_p13:\*
- 13: gb\_ro:\*
- 14: gb\_st:\*
- 15: gb\_sy:\*
- 16: gb\_un:\*
- 17: gb\_v1:\*
- 18: gb\_hcg:\*
- 19: em\_ba:\*
- 20: em\_fun:\*
- 21: em\_hum1:\*
- 22: em\_hum2:\*
- 23: em\_in:\*
- 24: em\_om:\*
- 25: em\_or:\*
- 26: em\_ov:\*
- 27: em\_pat:\*
- 28: em\_ph:\*
- 29: em\_pl:\*
- 30: em\_ro:\*
- 31: em\_sy:\*
- 32: em\_un:\*
- 33: em\_v1:\*
- 34: em\_hcg:\*
- 35: em\_sts:\*
- 36: gb\_bal:\*
- 37: gb\_ba2:\*
- 38: gb\_p11:\*
- 39: gb\_p12:\*
- 40: gb\_p1:\*
- 41: gb\_p12:\*
- 42: gb\_p13:\*
- 43: gb\_sts:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No. Query Match Score Length DB ID Description

1	5711	100.0	5711	6	AR007334
2	5709.4	100.0	5914	6	AR004673
3	5709.4	100.0	5914	6	AR008159
4	5709.4	100.0	5914	6	I76943
5	5709.4	100.0	5914	6	I80938
6	5709.4	100.0	5914	6	I81034
7	5709.4	100.0	5711	10	HSU14680
8	5709.4	100.0	5711	40	HSU14680
9	5707.8	99.9	5711	6	I40795
10	5707.8	99.9	5711	6	I40801
11	5703	99.9	5711	6	AR007335
12	5701.4	99.8	5711	6	AR007333
13	5701.4	99.8	5711	6	I59546
14	5698.4	99.8	5712	6	I40803
15	5697.4	99.8	5710	6	I40797
16	5695.4	99.7	5709	6	I40793
17	5695.4	99.7	5709	6	I40798
18	5695.4	99.7	5709	6	I40799
19	5695.4	99.7	5709	6	I40800
20	5691.4	99.7	5707	6	I40802
21	5655.4	99.0	5689	6	I40794
22	5629.2	98.6	5770	6	I40796
23	5590.4	97.9	5656	6	I40792
24	5532.4	96.9	5693	11	AF005068
25	5532.4	96.9	5693	41	AF005068
26	5387.6	69.8	5637	4	CFU50709
27	3427.4	60.0	117143	12	HUMBCAL
28	3427.4	60.0	117143	42	HUMBCAL
29	3412.2	59.7	4249	6	AR004691
30	3412.2	59.7	4249	6	AR008177
31	3412.2	59.7	4249	6	I76961
32	3412.2	59.7	4249	6	I80956
33	3412.2	59.7	4249	6	I81052
34	3382.8	59.2	3426	12	AF019075
35	3382.8	59.2	3426	42	AF019075
36	3378	59.1	3426	12	AF019076
37	3378	59.1	3426	12	AF019076
38	3326.8	58.3	3426	12	AF019077
39	3326.8	58.3	3426	12	AF019077
40	3165	55.4	3423	12	AF019078
41	3165	55.4	3423	12	AF019078
42	2940.2	51.5	3441	12	AF019079
43	2940.2	51.5	3441	12	AF019079
44	2804.4	49.1	5607	13	AF036760
45	2748.2	48.1	5702	13	MMU31625

## ALIGNMENTS

RESULT 1  
LOCUS AR007334 5711 bp DNA  
DEFINITION AR007334 Sequence 3 from patent US 5750400  
ACCESSION AR007334  
KEYWORDS 93966818  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,  
Scheller,D.B. and Zeng,B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 5750400-A 3 12-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1956 a 1098 c 1274 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;



QY	2161	GTACAGCCAAATGAAACACACAGTAATAAAGACATGACGGCATCTTTCCAGAGCTGA	2220
Db	2161	GTACAAACCCAAATGAAGAACACAAAGTAAGAAAGATGACAGCATCTTTCCAGAGCTGA	2220
QY	2221	AGTTAAACAAATGACACCGTGTTCTTTTACTAATGAGTGCAAATATCCAGTGAACCTTAAAGAT	2280
Db	2221	AGTTAAACAAATGACACCGTGTTCTTTTACTAATGAGTTCAAATATCCAGTGAACCTTAAAGAT	2280
QY	2281	TTGTCAATCCTAGCCCTTCACAGAGAAAGAAAAGAGAAATAGAAAACAGTTAAAGTG	2340
Db	2281	TTGTCAATCCTAGCCCTTCACAGAGAAAGAAAAGAGAAATAGAAAACAGTTAAAGTG	2340
QY	2341	CTAATAATGCTGAAGACCCCAAGAATCTACTGTAAAGTGGAAAAAGGTTTGGCAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGAATCTACTGTAAAGTGGAAAAAGGTTTGGCAACTG	2400
QY	2401	AAAGATCTGTAGAGTAGACAGTATTTTCATTTGGTACTGTAAGTATGAGCACTGAG	2460
Db	2401	AAAGATCTGTAGAGTAGACAGTATTTTCATTTGGTACTGTAAGTATGAGCACTGAG	2460
QY	2461	AAAGTATCTGTTACTGTGAAGTTAGCACTCTAGGGAAGCCAAAAACAGACCATAATAT	2520
Db	2461	AAAGTATCTGTTACTGTGAAGTTAGCACTCTAGGGAAGCCAAAAACAGACCATAATAT	2520
QY	2521	GTGTAGACAGTGTGCAGCAATTTGAAACCACCAAGGAGTAATTTATGTTGTTCACAA	2580
Db	2521	GTGTAGACAGTGTGCAGCAATTTGAAACCACCAAGGAGTAATTTATGTTGTTCACAA	2580
QY	2581	ATTAATAGAAATGACACAGAGGCTTTTAAGTATTCATTTGGACATGAAAGTTAAACACAGTC	2640
Db	2581	ATTAATAGAAATGACACAGAGGCTTTTAAGTATTCATTTGGACATGAAAGTTAAACACAGTC	2640
QY	2641	GGGAACAACAGATGTGAATGGAAGGAAGTAAGTAAGTATGAGTATTTGGAGAAATCAT	2700
Db	2641	GGGAACAACAGATGTGAATGGAAGGAAGTAAGTAAGTATGAGTATTTGGAGAAATCAT	2700
QY	2701	TCAAGGTTTCAAAACGGCCAGCTCATTTTGCTGTGTTTCAAAATCCAGGAATCCAGAGAGG	2760
Db	2701	TCAAGGTTTCAAAACGGCCAGCTCATTTTGCTGTGTTTCAAAATCCAGGAATCCAGAGAGG	2760
QY	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGTCCTTAAAGAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGTCCTTAAAGAACAAAGTCCAAAAGTCACTT	2820
QY	2821	TTGATGTGAACAAAGAGAGAAATCAAGAGAAAGATAGTCTAATATCAAGGCTGATC	2880
Db	2821	TTGATGTGAACAAAGAGAGAAATCAAGAGAAAGATAGTCTAATATCAAGGCTGATC	2880
QY	2881	AGACAGTTAATATCATCTGCAGGCTTTCTGTGGTTGTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCATCTGCAGGCTTTCTGTGGTTGTCAGAAAGATTAAGCCAGTTGATA	2940
QY	2941	ATGGCAATGTAGATATCAAGAGAGGCTGTAGGTTTGTGCTATCATCTAGTTCAGAGCA	3000
Db	2941	ATGGCAATGTAGATATCAAGAGAGGCTGTAGGTTTGTGCTATCATCTAGTTCAGAGCA	3000
QY	3001	ACGAAGATGACATCTATTCTCCAAATTAACATGAGCTTTTACAAAAACCCATATGCTATAC	3060
Db	3001	ACGAAGATGACATCTATTCTCCAAATTAACATGAGCTTTTACAAAAACCCATATGCTATAC	3060
QY	3061	CACACATTTTCCCATCAATCATTTTGTAAAACTTAATGTAAAGAAAATCTGTAGAGG	3120
Db	3061	CACACATTTTCCCATCAATCATTTTGTAAAACTTAATGTAAAGAAAATCTGTAGAGG	3120
QY	3121	AAAACTTTSAGAGAACTTCAATGTCACTGGAAGAGAAATGGGAATGAGAAACTTCCAA	3180
Db	3121	AAAACTTTSAGAGAACTTCAATGTCACTGGAAGAGAAATGGGAATGAGAAACTTCCAA	3180
QY	3181	GTACAGTGAGACCAATTAGCCGTAATPACATTAGAGAAAATGTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAGACCAATTAGCCGTAATPACATTAGAGAAAATGTTTAAAGAGCCAGCT	3240

QY	3241	CAGCAATATTAAAGATAGGTTCCAGTACTATATATAAGTGGGCTCCAGTATTAAATGAA	3300
Db	3241	CAGCAATATTAAAGATAGGTTCCAGTACTATATATAAGTGGGCTCCAGTATTAAATGAA	3300
QY	3301	TAGGTTCCAGTATGAAGAAACCTTCACAGACAACTAGTGTGAACAGAGGGCCCAAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAGAAACCTTCACAGACAACTAGTGTGAACAGAGGGCCCAAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGGCAACCTGAGGCTATATAACAAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGGCAACCTGAGGCTATATAACAAAGTCTTCTGGAA	3420
QY	3421	GTAATTGTAGCAATCGGAATAAAAAAGCAAGATATGAGAAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATTGTAGCAATCGGAATAAAAAAGCAAGATATGAGAAGTAGTTCAGACTGTTA	3480
QY	3481	ATACGATTTCCTCCATCTGATTCGATTTCAGATTAACATGAGCTATAGGAACTATCTC	3540
Db	3481	ATACGATTTCCTCCATCTGATTCGATTTCAGATTAACATGAGCTATAGGAACTATCTC	3540
QY	3541	ATGCATCTCAGGTTGTGTTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTGTGTTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGG	3600
QY	3601	AAGATATGATTGTTGCTGAATAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAACCG	3660
Db	3601	AAGATATGATTGTTGCTGAATAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAACCG	3660
QY	3661	TCCAGAAAGGAGACCTTAGACAGAGAGTCTGAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGGAGACCTTAGACAGAGAGTCTGAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGCCAAGAAATAGAGTCCTCAGAAAGAACTTATCTAGTAGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATAGAGTCCTCAGAAAGAACTTATCTAGTAGAGATG	3780
QY	3781	AAGAGCTTCCTGCTTCCAACTCTGTTATTGTTAAAGTAAACAAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCTGCTTCCAACTCTGTTATTGTTAAAGTAAACAAATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGACACCGTGTCTACGAGTGTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGACACCGTGTCTACGAGTGTGTCTTAAGAACACAGAGAGAAATTTAT	3900
QY	3901	TATCTTTGAAGAAATAGCTTTAAATGACGTGCGATACAGGTATATTTGGCAAAAGCATCTC	3960
Db	3901	TATCTTTGAAGAAATAGCTTTAAATGACGTGCGATACAGGTATATTTGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTCTGCTAGCTGTGTTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTCTGCTAGCTGTGTTTTCTTCACAGTCA	4020
QY	4021	GTTGAATTGGAAGACTTACATCTGCAAAATACAAACCCAGAGATCTTTCTTGATTTGCTTT	4080
Db	4021	GTTGAATTGGAAGACTTACATCTGCAAAATACAAACCCAGAGATCTTTCTTGATTTGCTTT	4080
QY	4081	CCAAACAAATAGGCATCACTGTGAAGAGCAGGGAATTTGTTGATGTGACAAAGAAATTTGG	4140
Db	4081	CCAAACAAATAGGCATCACTGTGAAGAGCAGGGAATTTGTTGATGTGACAAAGAAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGGAAGCGGCTTGGAAAGAAATATATAGAGAGCAAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAGCGGCTTGGAAAGAAATATATAGAGAGCAAAAGCA	4200
QY	4201	TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAGAAACAGCGCTCTGAGG	4260
Db	4201	TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAGAAACAGCGCTCTGAGG	4260
QY	4261	ACTGCTAAGGGCTACTCTCTCAGAGTGAACATTTTAAACCTAGAGAGGGATACCAATGC	4320
Db	4261	ACTGCTAAGGGCTACTCTCTCAGAGTGAACATTTTAAACCTAGAGAGGGATACCAATGC	4320
QY	4321	AACATTAACCTGATTAAGCTTCACAGAGAAATGGCTGAATCAAACTGTGTTAAACAGC	4380

```

Db 4321 AACATAACCTGATAACTCCAGACGAAATGGCTGAACCTGATGAAAGCTGTAGAACAGC 4380
OY 4381 ATGGAGCCAGCCTTCTACAGCTACCTTCATCATATAAGTACTCTGTGCCCCCTGAG 4440
Db 4381 ATGGAGCCAGCCTTCTACAGCTACCTTCATCATATAAGTACTCTGTGCCCCCTGAG 4440
OY 4441 ACCTGCAAAATCCAGAAACAAAGACATGAAAAAGCAGTATTAACTTCACAGAAAGTA 4500
Db 4441 ACCTGCAAAATCCAGAAACAAAGACATGAAAAAGCAGTATTAACTTCACAGAAAGTA 4500
OY 4501 GTGAATACCTTATAGCAGAAATCCAGAGGCTTTGCTGCGACAAAGTTGAGGTGTG 4560
Db 4501 GTGAATACCTTATAGCAGAAATCCAGAGGCTTTGCTGCGACAAAGTTGAGGTGTG 4560
OY 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGTGAAGAGTGCATCCCTCTTAAT 4620
Db 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGTGAAGAGTGCATCCCTCTTAAT 4620
OY 4621 GCCCATCATTAAGATGATAGTGTGATGACAGTGTGCTGCGAGTCTTGAGAAATAGAA 4680
Db 4621 GCCCATCATTAAGATGATAGTGTGATGACAGTGTGCTGCGAGTCTTGAGAAATAGAA 4680
OY 4681 ACTACCATGTCAGAGAGAGGCTCATTAAGTGTGATGATGAGAGACAGAGCTGAGAG 4740
Db 4681 ACTACCATGTCAGAGAGAGGCTCATTAAGTGTGATGATGAGAGACAGAGCTGAGAG 4740
OY 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTCCAAAGCAGAGATAGAGGAA 4800
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTCCAAAGCAGAGATAGAGGAA 4800
OY 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTTCTGATGACCCCTGATCTGATCTCTG 4860
Db 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTTCTGATGACCCCTGATCTGATCTCTG 4860
OY 4861 AAGCAGAGGCCCCGAGATGAGCTGTGTGCAACATACATCTTCAACCTGATCTGATGA 4920
Db 4861 AAGCAGAGGCCCCGAGATGAGCTGTGTGCAACATACATCTTCAACCTGATCTGATGA 4920
OY 4921 AAGTCCCCCAATGAAAGTGTGCAAGATCTGCCAGAGTCCAGCTGCTGCTATCTACTG 4980
Db 4921 AAGTCCCCCAATGAAAGTGTGCAAGATCTGCCAGAGTCCAGCTGCTGCTATCTACTG 4980
OY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGACCAATTTGACAG 5040
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGACCAATTTGACAG 5040
OY 5041 CTTCACAGAGAAAGGCTCAACAAAAGATGTCATGTGTGCTGCGCTGACCCAGAG 5100
Db 5041 CTTCACAGAGAAAGGCTCAACAAAAGATGTCATGTGTGCTGCGCTGACCCAGAG 5100
OY 5101 AATTATGCTGCTGTACAGATTTGCCAGAAAACACACATCACTTTAACTAATTA 5160
Db 5101 AATTATGCTGCTGTACAGATTTGCCAGAAAACACACATCACTTTAACTAATTA 5160
OY 5161 CTGGAAGAGTACTCATGTGTGTTATGAAAACAGTGTGCTGAGTGTGCTGAGGAGAC 5220
Db 5161 CTGGAAGAGTACTCATGTGTGTTATGAAAACAGTGTGCTGAGTGTGCTGAGGAGAC 5220
OY 5221 TGAATATTTTCTAGGAATTTGCCGAGAGAAATGGGTAGTATTTTCCGGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATTTGCCGAGAGAAATGGGTAGTATTTTCCGGGTGACCC 5280
OY 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAAATG 5340
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAAATG 5340
OY 5341 TCATATGGAAGAAACCAAGAGTCCAAAGGAGCAGAGAGATCCCAAGAGAGATCT 5400
Db 5341 TCATATGGAAGAAACCAAGAGTCCAAAGGAGCAGAGAGATCCCAAGAGAGATCT 5400
OY 5401 TCAGGGGGCTAGAAATCTGTGATGAGGCTTACCAACATGCCCAGATCAATG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTGATGAGGCTTACCAACATGCCCAGATCAATG 5460

```

```

Db 5401 TCAGGGGGCTAGAAATCTGTGATGAGGCTTACCAACATGCCCAGATCAATG 5460
OY 5461 AATGATGATGACAGCTGTGTGCTGCTGTGTGTAAGAGAGTTCATCATCACCCTTG 5520
Db 5461 AATGATGATGACAGCTGTGTGCTGCTGTGTGTAAGAGAGTTCATCATCACCCTTG 5520
OY 5521 GCACAGGTGTCCACCAATTTGTGTGTGTCAGCAGCAGATGCTGTGAGAGAGATGCT 5580
Db 5521 GCACAGGTGTCCACCAATTTGTGTGTGTGTCAGCAGCAGATGCTGTGAGAGAGATGCT 5580
OY 5581 TCCATGCAATTTGGCAGATGATGTGAGGACCTGTGAGGACCGAGAGTGGTGTGACA 5640
Db 5581 TCCATGCAATTTGGCAGATGATGTGAGGACCTGTGAGGACCGAGAGTGGTGTGACA 5640
OY 5641 GTTAGCAGCTCTACCAAGTGCAGAGAGCTGAGACACTACCTGATACCCAGATCCCA 5700
Db 5641 GTTAGCAGCTCTACCAAGTGCAGAGAGCTGAGACACTACCTGATACCCAGATCCCA 5700
OY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 2
AR004673 AR004673 5914 bp DNA PAT 04-DEC-1998
LOCUS Sequence 1 from patent US 5747282.
DEFINITION AR004673
ACCESSION 93965552
NID
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 5914)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamp,A.,
Harsman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P. Andrew.
170-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5747282-A 1 05-MAY-1998;
FEATURES Location/Qualifiers
source 1..5914
BASE COUNT 2006 a 1156 c 1316 g 1436 t
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 AGCTCGCTGAGACTTCTGTGACCCGACACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Db 1 AGCTCGCTGAGACTTCTGTGACCCGACACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
OY 61 CTTGCGCTCAGAGGCTTACCCCTGCTGCTGTGGTAAAGTTCATTGTGGAACGAAAGAAA 120
Db 61 CTTGCGCTCAGAGGCTTACCCCTGCTGCTGTGGTAAAGTTCATTGTGGAACGAAAGAAA 120
OY 121 TGGATTAATCTGCTTCTGCGGTGGAAGAGTACAAAATGCTAATAGCTATGACGAAAA 180
Db 121 TGGATTAATCTGCTTCTGCGGTGGAAGAGTACAAAATGCTAATAGCTATGACGAAAA 180
OY 181 TCTTAGAGTCCCATCTGCTGTGAGTGTATCAAGAGAACCTGTCTCCAAAGTGTGACC 240
Db 181 TCTTAGAGTCCCATCTGCTGTGAGTGTATCAAGAGAACCTGTCTCCAAAGTGTGACC 240
OY 241 ACAATATTTTCAAAATTTTGCAGCTGAACCTTCTCAACGAGAAAGAGGCTTACAGT 300
Db 241 ACAATATTTTCAAAATTTTGCAGCTGAACCTTCTCAACGAGAAAGAGGCTTACAGT 300
OY 301 GTCCTTATGATAGATGATATTAACCAAGAGGCTTACAAAGAGTACGATTTAGTC 360
Db 301 GTCCTTATGATAGATGATATTAACCAAGAGGCTTACAAAGAGTACGATTTAGTC 360

```



QY	1441	TATGTAAAGTGAAGGTTCTACTCCAAATCAGTAGAGATTAATTTGAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGGTTCTACTCCAAATCAGTAGAGATTAATTTGAGACAAATAT	1500
QY	1501	TTGGGAAACCTATTCGGAGAGAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAATC	1560
Db	1501	TTGGGAAACCTATTCGGAGAGAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAATC	1560
QY	1561	TAAATATGAGAGCATTTGTTACTGAGCAGATTAATTAACAAAGGTCCTCCACAAATA	1620
Db	1561	TAAATATGAGAGCATTTGTTACTGAGCAGATTAATTAACAAAGGTCCTCCACAAATA	1620
QY	1621	AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCATCTTGAAGATTTTATCAAGAA	1680
Db	1621	AATTAAAGCTTAAAGAGAGACCTTACATCAGGCTTCATCTTGAAGATTTTATCAAGAA	1680
QY	1681	CAGATTGGGAGTTCAAAACAGCTCGAAATGTAATATGAGGAATTAACCAAGGAGC	1740
Db	1681	CAGATTGGGAGTTCAAAACAGCTCGAAATGTAATATGAGGAATTAACCAAGGAGC	1740
QY	1741	AGAAAGCTCAAGTATGAATTAATTAATATGATGATGATGATTAACAAAGGTGAT	1800
Db	1741	AGAAAGCTCAAGTATGAATTAATTAATATGATGATGATGATTAACAAAGGTGAT	1800
QY	1801	CTATTCAAGATGAGAAAAATCCTAACCCATAGATCACTCGAAAAAGATCTGTTCA	1860
Db	1801	CTATTCAAGATGAGAAAAATCCTAACCCATAGATCACTCGAAAAAGATCTGTTCA	1860
QY	1861	AAAGGAAGCTGAACCTTAAGCAGCATTAAGCATATGSACTCGAATTTAAATATCC	1920
Db	1861	AAAGGAAGCTGAACCTTAAGCAGCATTAAGCATATGSACTCGAATTTAAATATCC	1920
QY	1921	ACAATTCAAAAAGCCTTAAAAAGATAGGCTGGAGGAGCTCTTCCACAGGCAATTC	1980
Db	1921	ACAATTCAAAAAGCCTTAAAAAGATAGGCTGGAGGAGCTCTTCCACAGGCAATTC	1980
QY	1981	ATGGCTTGAATAGTAGTAGTGAAGAAATCTAAGCCACCTATTTGTACTGAATGCAAA	2040
Db	1981	ATGGCTTGAATAGTAGTAGTGAAGAAATCTAAGCCACCTATTTGTACTGAATGCAAA	2040
QY	2041	TTGATATGTTGTTCTACGACATGAAGAGATTAAGAAAAAAAGTACAAACAATGCCATCA	2100
Db	2041	TTGATATGTTGTTCTACGACATGAAGAGATTAAGAAAAAAAGTACAAACAATGCCATCA	2100
QY	2101	GGCAGAGAGAAACCTCAACTCATGATGGAAGGTAAAGAACCTGCAACTGAGGCAAGAA	2160
Db	2101	GGCAGAGAGAAACCTCAACTCATGATGGAAGGTAAAGAACCTGCAACTGAGGCAAGAA	2160
QY	2161	GTAACAAGCCAAATGACAACAAGTAAAGAAAGATGACAGCTACTTCCACAGCTGA	2220
Db	2161	GTAACAAGCCAAATGACAACAAGTAAAGAAAGATGACAGCTACTTCCACAGCTGA	2220
QY	2221	AGTTAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATACAGTAACCTTAAAGAT	2280
Db	2221	AGTTAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATACAGTAACCTTAAAGAT	2280
QY	2281	TTTGATATCCTAGCTCTTCCAAAGAGAAAGAAAGAGAGAAATATBAAAACAGTTAAAGT	2340
Db	2281	TTTGATATCCTAGCTCTTCCAAAGAGAAAGAAAGAGAGAAATATBAAAACAGTTAAAGT	2340
QY	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTGAAGTGAAGAGGCTTTTGCAAATG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTGAAGTGAAGAGGCTTTTGCAAATG	2400
QY	2401	AAAGATCTGTAAGAGTAGAGCATTAATTCATGTGTACCTGGTACTGATTATGGAACCTAGG	2460
Db	2401	AAAGATCTGTAAGAGTAGAGCATTAATTCATGTGTACCTGGTACTGATTATGGAACCTAGG	2460
QY	2461	AAATATATCTGTTACATGGAAGTGAAGCATCTCTAGGGAAGGCAAAAACAACCAATTAAT	2520
Db	2461	AAATATATCTGTTACATGGAAGTGAAGCATCTCTAGGGAAGGCAAAAACAACCAATTAAT	2520
QY	2521	GTTGATCTAGTGTGAGCATTTTGAAGAAACCCCAAGGAGATTAATCATGTTGTGTCCAAAG	2580

|||||  
Db 2521 GTGAGTCAGTGTGACACATTTGAAAACCCAGAGGACTAATTCATGTTGTTCCAAAG 2580  
OY 2581 ATATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGTC 2640  
Db 2581 ATATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGTC 2640  
OY 2641 GGGAAACAGCATGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGCAAGTACAT 2700  
Db 2641 GGGAAACAGCATGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGCAAGTACAT 2700  
OY 2701 TCAAGGTTTCAAGGGCCAGTCATTTGCTGTTTCAAAATCAGGAATGAGAGAGAG 2760  
Db 2701 TCAAGGTTTCAAGGGCCAGTCATTTGCTGTTTCAAAATCAGGAATGAGAGAGAG 2760  
OY 2761 AATGTCGAACATTCCTCTGCTCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCAC 2820  
Db 2761 AATGTCGAACATTCCTCTGCTCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCAC 2820  
OY 2821 TTGAAATGGAACAAAGGAAGAAATCAAGGAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAAATGGAACAAAGGAAGAAATCAAGGAAGATGAGTCTAATATCAAGCCTGTAC 2880  
OY 2881 AGACAGTTAATATCATCTCAGGCTTCTGCTGTTGTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCATCTCAGGCTTCTGCTGTTGTCAGAAAGATAAGCCAGTTGATA 2940  
OY 2941 ATGCCAAATGATGATCAAAAGAGGCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Db 2941 ATGCCAAATGATGATCAAAAGAGGCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
OY 3001 ACGAACTGAGCTGATTCCTCAAAATAACATGACTTTTCAAAACCCTATCTGTATAC 3060  
Db 3001 ACGAACTGAGCTGATTCCTCAAAATAACATGACTTTTCAAAACCCTATCTGTATAC 3060  
OY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACATAATGTAGAAAAATCTGTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACATAATGTAGAAAAATCTGTAGAG 3120  
OY 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAAGAAATGGGAATGAGAACATTCGA 3180  
Db 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAAGAAATGGGAATGAGAACATTCGA 3180  
OY 3181 GTACAGTACACAAATTAAGCCGTATATACATTAGAGAAATGTTTAAAGAACGACGT 3240  
Db 3181 GTACAGTACACAAATTAAGCCGTATATACATTAGAGAAATGTTTAAAGAACGACGT 3240  
OY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300  
OY 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGGAACTAGTGAAGAACAGAGGCCCAAAATGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGGAACTAGTGAAGAACAGAGGCCCAAAATGA 3360  
OY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTATTAACAAAGTCTCTCGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTATTAACAAAGTCTCTCGAA 3420  
OY 3421 GTAATTTAAGCATCTGGAATTAAGAAAGCAAGATATGAAGATAGTTCAGACTGTTA 3480  
Db 3421 GTAATTTAAGCATCTGGAATTAAGAAAGCAAGATATGAAGATAGTTCAGACTGTTA 3480  
OY 3481 ATACAGATTTCTCTCATATCTGATTTCACTAGTAAGAACAGCCCTATGGAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTCACTAGTAAGAACAGCCCTATGGAGTAGTC 3540  
OY 3541 ATGCAATCTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGTTGAAATGAAG 3600  
Db 3541 ATGCAATCTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGTTGAAATGAAG 3600  
OY 3601 AAGATCTAGTTTGTGAAATGACATTAAGAAAGTTCGCTGTTTAAAGCAAGCG 3660  
|||||

Db 3601 AAGATCTAGTTTGTGCTAATAATGACATTAAGGAAAGTCTGCTGTTTAAAGCAAAAGCG 3660  
OY 3661 TCCAGAAAGAGAGGCTTAGACAGAGGCTCTAGCCCTTTCACCATATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGAGGCTTAGACAGAGGCTCTAGCCCTTTCACCATATACATTTGGCTCAGG 3720  
OY 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCTCTCAGAAAGAACTTTATCTAGTAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCTCTCAGAAAGAACTTTATCTAGTAGATG 3780  
OY 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTGGTAAAGTAAACATAATCCTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTGGTAAAGTAAACATAATCCTCTCAGT 3840  
OY 3841 CTACTAGGCAATAGCACCGCTTCTACCGAGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGGCAATAGCACCGCTTCTACCGAGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
OY 3901 TATCATTTAAGAAATAGCTTAATATGACTGCACTAACACAGTAAATTTGGCAAAAGCATCTC 3960  
Db 3901 TATCATTTAAGAAATAGCTTAATATGACTGCACTAACACAGTAAATTTGGCAAAAGCATCTC 3960  
OY 3961 AGGAACATCACCTTAGTAGAGGAAACAAATGTCTGCTAGCTGTTTCTTCAAGTGA 4020  
Db 3961 AGGAACATCACCTTAGTAGAGGAAACAAATGTCTGCTAGCTGTTTCTTCAAGTGA 4020  
OY 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGTCTTCTGTTGATGGTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGTCTTCTGTTGATGGTCTT 4080  
OY 4081 CCAAAACAAATGAGGATGATGCTGAAGGCCAGGAGTGGCTGAGAGGACAAAGAAATGG 4140  
Db 4081 CCAAAACAAATGAGGATGATGCTGAAGGCCAGGAGTGGCTGAGAGGACAAAGAAATGG 4140  
OY 4141 TTTGAGATGATGAAGAAAGAGAAAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Db 4141 TTTGAGATGATGAAGAAAGAGAAAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
OY 4201 TGGATTCAACTTAGTGAAGACACATCTGGGTTGAGAGTGAAGAAAGAGCTCTGTAAG 4260  
Db 4201 TGGATTCAACTTAGTGAAGACACATCTGGGTTGAGAGTGAAGAAAGAGCTCTGTAAG 4260  
OY 4261 ACTGCTAGGGGCTATCCCTCTGAGAGTACATTTTAACCATCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTAGGGGCTATCCCTCTGAGAGTACATTTTAACCATCAGCAGAGGATACCATGC 4320  
OY 4321 AACATTAACCTGATTAAGGCTCCAGCAGGAAATGAGCTGAAGAGCTGTGTAAGACAGC 4380  
Db 4321 AACATTAACCTGATTAAGGCTCCAGCAGGAAATGAGCTGAAGAGCTGTGTAAGACAGC 4380  
OY 4381 ATGGAGCCAGCCTTCTAACAGCTACCTTCCATCATTAAGTGAATCTTGCCTTGAGG 4440  
Db 4381 ATGGAGCCAGCCTTCTAACAGCTACCTTCCATCATTAAGTGAATCTTGCCTTGAGG 4440  
OY 4441 ACCTGCGAAATTCAGAACAAAGCAGATCAGAAAAAGCAGATTAATCTTCACAGAAAAAGTA 4500  
Db 4441 ACCTGCGAAATTCAGAACAAAGCAGATCAGAAAAAGCAGATTAATCTTCACAGAAAAAGTA 4500  
OY 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTCTGCTGCAAGTGTGAGTGCTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTCTGCTGCAAGTGTGAGTGCTG 4560  
OY 4561 CAGATAGTTCTTACAGTAAATAATTAAGAACAGAGTGAAGAGGTATCCCTTTTAAT 4620  
Db 4561 CAGATAGTTCTTACAGTAAATAATTAAGAACAGAGTGAAGAGGTATCCCTTTTAAT 4620  
OY 4621 GCCCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
Db 4621 GCCCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
OY 4681 ACTACCCATCTCAAGAGAGAGCTCATTAAGGTTGTTGATGAGAGGACACACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGAGAGCTCATTAAGGTTGTTGATGAGAGGACACACAGCTGGAAG 4740

DEFINITION	Sequence 1 from patent US 5753441.
ACCESSION	AB008159
NID	93967268
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 5914)
AUTHORS	Skolnick,M.R., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A., Hershan,K.D., Shattuck-Eidens,D.M., Tavtiglian,S.V., Wiseman,R.W., and Futreal,P.Andrew, 170-linked breast and ovarian cancer susceptibility gene Patent: US 5753441-A 1 19-MAY-1998; Location/Qualifiers 1..5914
TITLE	
JOURNAL	
FEATURES	
BASE COUNT	2006 a 1156 c 1316 g 1436 t
ORIGIN	/organism="unknown"
Query Match	100.0%; Score 5709.4; DB 6; Length 5914;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 5710; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 AGCTGCGTAGACCTTCCTGGAACCCCGCACACAGCGCTGTGGGTTCTCAGATPACTGGGCC 60
DB	1 AGCTGCGTAGACCTTCCTGGAACCCCGCACACAGCGCTGTGGGTTCTCAGATPACTGGGCC 60
QY	61 CCTGGCGTCAGAGGCCCTCAACCCCTCCTCGGCTAAGTTCAATGGACAGAAAGAA 120
DB	61 CCTGGCGTCAGAGGCCCTCAACCCCTCCTCGGCTAAGTTCAATGGACAGAAAGAA 120
QY	121 TGGATTATCTGCTCTTCCGCTTGAGAAAGTACAAATATGATTATCTATGACAGAAA 180
DB	121 TGGATTATCTGCTCTTCCGCTTGAGAAAGTACAAATATGATTATCTATGACAGAAA 180
QY	181 TCTTAGAGTGTCCACTGCTGTGTGAGTTGATCAAGAAACCTGTCTCCACAAAGTGTGACC 240
DB	181 TCTTAGAGTGTCCACTGCTGTGTGAGTTGATCAAGAAACCTGTCTCCACAAAGTGTGACC 240
QY	241 ACATATTTTGCAGAAATTTTGCAATGCTGCGAATCTTCACACAGAAAGGAGGCTTCACAGT 300
DB	241 ACATATTTTGCAGAAATTTTGCAATGCTGCGAATCTTCACACAGAAAGGAGGCTTCACAGT 300
QY	301 GTCCCTTATGTAGAAATGATATTAACCAAAAGAGGCTTCAGAAAGTACGATTAGTC 360
DB	301 GTCCCTTATGTAGAAATGATATTAACCAAAAGAGGCTTCAGAAAGTACGATTAGTC 360
QY	361 AACTGTGTGAAGAGCTATGTGAAAATCATTTTGTGCTTTCAGCTTGACACAGAGTTGGAGT 420
DB	361 AACTGTGTGAAGAGCTATGTGAAAATCATTTTGTGCTTTCAGCTTGACACAGAGTTGGAGT 420
QY	421 ATGCAACAGCTATTAATTTGCAAAAAAGGAAAATTAAGTCTCGAATCATTAAGATG 480
DB	421 ATGCAACAGCTATTAATTTGCAAAAAAGGAAAATTAAGTCTCGAATCATTAAGATG 480
QY	481 AAGTTTCTATCATCAAAAGTATGGGCTACAAAAACCGTCCAAAAAGAGTTCTTACAGAGT 540
DB	481 AAGTTTCTATCATCAAAAGTATGGGCTACAAAAACCGTCCAAAAAGAGTTCTTACAGAGT 540
QY	541 AACCGGAAATCTCTTCCCTTGAGAGAAACCAAGTCTCAGTCCAACTCTTAACCTTGGAA 600
DB	541 AACCGGAAATCTCTTCCCTTGAGAGAAACCAAGTCTCAGTCCAACTCTTAACCTTGGAA 600
QY	601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATACCAACCTCAAAAAGCGTGTCTACATTTG 660
DB	601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATACCAACCTCAAAAAGCGTGTCTACATTTG 660
QY	661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCGAGTGGAG 720
DB	661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCGAGTGGAG 720
QY	721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGACACAGGAGTGAATCAGTTTGGATTCTG 780

|||||  
Db 721 ATCAAGATTGTTACAAATCACCCCTCAAGGAACCAAGGATGAATTCAGTTGGATTTCG 780  
QY 781 CAAAAAGGCGCTTGTAAATTTCTGAGAGGATGTAACAATCTGAACATCATCAAC 840  
Db 781 CAAAAAGGCGCTTGTAAATTTCTGAGAGGATGTAACAATCTGAACATCATCAAC 840  
QY 841 CCACTAATATGATTTGGAACACCACTGAGAAAGCTGAGAGGATCCAGAAAAGT 900  
Db 841 CCACTAATATGATTTGGAACACCACTGAGAAAGCTGAGAGGATCCAGAAAAGT 900  
QY 901 ATCAGGAGATGCTGTTCAAACTGCAATGAGGACCATGTCGCAAAATATCATGCCA 960  
Db 901 ATCAGGAGATGCTGTTCAAACTGCAATGAGGACCATGTCGCAAAATATCATGCCA 960  
QY 961 GCTCATTAACAGCATGAGAACAGCAGTTATTACTACTAAGACAGAAATGATGAGAA 1020  
Db 961 GCTCATTAACAGCATGAGAACAGCAGTTATTACTACTAAGACAGAAATGATGAGAA 1020  
QY 1021 AGGCTGAATTCGTAAATAAAAGCAAAAGCCTGCTTAGCAAGAGCCAAATACAGAT 1080  
Db 1021 AGGCTGAATTCGTAAATAAAAGCAAAAGCCTGCTTAGCAAGAGCCAAATACAGAT 1080  
QY 1081 GGGCTGGAAGTAAGGAACATGATATGATGGCGGACTCCCGACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAGGAACATGATATGATGGCGGACTCCCGACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAAAGATGGAATAGAGAAAAGTCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAAAGATGGAATAGAGAAAAGTCCATGCT 1200  
QY 1201 CAGCAATCTAGAGATACGAGATGTTCTTGATTAACACTAAATAGCAGATTCAGA 1260  
Db 1201 CAGCAATCTAGAGATACGAGATGTTCTTGATTAACACTAAATAGCAGATTCAGA 1260  
QY 1261 AAGTAATGATGGTTTCCAGAGTGAATGTAAGTGGTCTGATGCTACATCATGATG 1320  
Db 1261 AAGTAATGATGGTTTCCAGAGTGAATGTAAGTGGTCTGATGCTACATCATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTGAATGAGAGTTTAAATGAGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTGAATGAGAGTTTAAATGAGTAGATG 1380  
QY 1381 AATATTCTGCTTCTCAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGCTTCTCAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTACTCTCAATCAGTAGAGATGAATTTGAAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTACTCTCAATCAGTAGAGATGAATTTGAAAGCAAAATAT 1500  
QY 1501 TTGGAAAAACCTATCGGAAGAGGACCTCCCACTTAAGCCATGTAATGAAAAATC 1560  
Db 1501 TTGGAAAAACCTATCGGAAGAGGACCTCCCACTTAAGCCATGTAATGAAAAATC 1560  
QY 1561 TAATTATAGGAGCAATTTGTTACTGAGCCAGATATACAGAGGCTCCCTCACAAATA 1620  
Db 1561 TAATTATAGGAGCAATTTGTTACTGAGCCAGATATACAGAGGCTCCCTCACAAATA 1620  
QY 1621 AATTAAGGCGTAAAGGAGACTCATGAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGGCGTAAAGGAGACTCATGAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCTCTGAATGATTAATCAGGGAATCAACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTCTGAATGATTAATCAGGGAATCAACCAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTATGAATTTACTATAGTGGTCAATGAGAAATCAAAAGGTGATT 1800  
Db 1741 AGAATGCTCAAGTATGAATTTACTATAGTGGTCAATGAGAAATCAAAAGGTGATT 1800  
QY 1801 CTATTGCAATGAGAAAAATCTAAACCAATAGATCATCGAAAAAAGATCTGTTCA 1860  
|||||

Db 1801 CTATTGCAATGAGAAAAATCTAAACCAATAGATCATCGAAAAAAGATCTGTTCA 1860  
QY 1861 AAACGAAGCTGAACCTTAAGCAGCAGTATTAACAATATGAACTGAATTAATATCC 1920  
Db 1861 AAACGAAGCTGAACCTTAAGCAGCAGTATTAACAATATGAACTGAATTAATATCC 1920  
QY 1921 ACAATTTCAAAAGCACTTAAAAAGATAGGCTGAGAGGAAGTCTTTACAGGCATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAAAAAGATAGGCTGAGAGGAAGTCTTTACAGGCATATTC 1980  
QY 1981 ATGGCTGAACCTGTAGTGTGTAAGTAATCAAGCCACCTAATTTACTGAATTTGCAA 2040  
Db 1981 ATGGCTGAACCTGTAGTGTGTAAGTAATCAAGCCACCTAATTTACTGAATTTGCAA 2040  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
QY 2101 GGCACAGCAAAACCTTACACTCATGGAAGTAAAGAACTGCATGAGCCAGAGA 2160  
Db 2101 GGCACAGCAAAACCTTACACTCATGGAAGTAAAGAACTGCATGAGCCAGAGA 2160  
QY 2161 GTAACCAAGCCAAATGAACAGCAAGTAAAGACATGACAGCATCTTCCAGAGCTGA 2220  
Db 2161 GTAACCAAGCCAAATGAACAGCAAGTAAAGACATGACAGCATCTTCCAGAGCTGA 2220  
QY 2221 AGTTAACCAATGACACTGTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2280  
Db 2221 AGTTAACCAATGACACTGTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2280  
QY 2281 TTGTCAATCTAGCCCTTCCAGAGAGAAAAAGAGAACTAGAAACGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCCTTCCAGAGAGAAAAAGAGAACTAGAAACGTTAAAGTGT 2340  
QY 2341 CTAATTAATGCTGAAGACCCCAAGATCATGTTAAATGAGAAAGGTTTCCAAACTG 2400  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCATGTTAAATGAGAAAGGTTTCCAAACTG 2400  
QY 2401 AAAGATCTGTAAGAGTAGCAGTATTTCAATGTTACTGTTATGAGCACTCAG 2460  
Db 2401 AAAGATCTGTAAGAGTAGCAGTATTTCAATGTTACTGTTATGAGCACTCAG 2460  
QY 2461 AAAGATCTGTTACTGGAAGTGAACCTAGGAGAAAGCAAAACCAATTAAT 2520  
Db 2461 AAAGATCTGTTACTGGAAGTGAACCTAGGAGAAAGCAAAACCAATTAAT 2520  
QY 2521 GTGTAGTCACTGTGACAGCATTTGAAACCCCAAGGACATTAATGATGTTCCAAAG 2580  
Db 2521 GTGTAGTCACTGTGACAGCATTTGAAACCCCAAGGACATTAATGATGTTCCAAAG 2580  
QY 2581 ATATAGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAATTAACACAGTC 2640  
Db 2581 ATATAGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAATTAACACAGTC 2640  
QY 2641 GGGAAACAGCATGGAATGGAAGAAAGTGAATGATGCTCAGTATTTGACAGATCAT 2700  
Db 2641 GGGAAACAGCATGGAATGGAAGAAAGTGAATGATGCTCAGTATTTGACAGATCAT 2700  
QY 2701 TCAAGGTTTCAAAAGCCGACAGTATGCTGTTTCCAAATCCAGGAAATGCGAAGAG 2760  
Db 2701 TCAAGGTTTCAAAAGCCGACAGTATGCTGTTTCCAAATCCAGGAAATGCGAAGAG 2760  
QY 2761 AATGTGCAACATTCCTGCCCACCTGCTGCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTCCTGCCCACCTGCTGCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
QY 2821 TTGAATGGAACAAAGAAAGAAATCAAGAAAGATGATGATTAATCAACCTGTAC 2880  
Db 2821 TTGAATGGAACAAAGAAAGAAATCAAGAAAGATGATGATTAATCAACCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGACAGGCTTCTGTTGTTGTCGAAGAAATGAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGACAGGCTTCTGTTGTTGTCGAAGAAATGAGCCAGTTGATA 2940  
|||||

QY	4021	GTGAATTGGAGAACTTACATCTGCAAAATPCCAACACCAGATCCTTTCTTGATTGGTTCTT	4080
Db	4021	GTGAATTGGAGAACTTACATCTGCAAAATPCCAACACCAGATCCTTTCTTGATTGGTTCTT	4080
QY	4081	CCAAACCAATAGGCATCAGTCTGAAAGCCAGGGATTTGCTGTAGTGCAGAGAAATGG	4140
Db	4081	CCAAACCAATAGGCATCAGTCTGAAAGCCAGGGATTTGCTGTAGTGCAGAGAAATGG	4140
QY	4141	TTTCAGATGATGAAGAAAGGAAAGCGGCTTGGAAACAAATATATAGAGAGCAAAACA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAAGCGGCTTGGAAACAAATATATAGAGAGCAAAACA	4200
QY	4201	TGGATTCAAACCTTGTGGTAAGCAGCATCTGGGTGTGAGAGTAAACAAAGCTCTGTAG	4260
Db	4201	TGGATTCAAACCTTGTGGTAAGCAGCATCTGGGTGTGAGAGTAAACAAAGCTCTGTAG	4260
QY	4261	ACTGCTCAGGGCTATCCTCTTCAGAGTGCATTTTAACCTCAGAGAGGGATTAACATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTTCAGAGTGCATTTTAACCTCAGAGAGGGATTAACATGC	4320
QY	4321	AACATTAACCTGATTAAGCCTCCAGCAGGAATAGGCTGAACTAGAACCTGTAGAACAGC	4380
Db	4321	AACATTAACCTGATTAAGCCTCCAGCAGGAATAGGCTGAACTAGAACCTGTAGAACAGC	4380
QY	4381	ATGGAGAGCAGCCTTCTTAACAGCTTACCCTTCATTAAGTACGCTTCTGCTCCCTTAGG	4440
Db	4381	ATGGAGAGCAGCCTTCTTAACAGCTTACCCTTCATTAAGTACGCTTCTGCTCCCTTAGG	4440
QY	4441	ACCTGCGAAATCCGAACAAAGCAACATCAGAAAACCAATATTAATCTTCACAGAAAAGTA	4500
Db	4441	ACCTGCGAAATCCGAACAAAGCAACATCAGAAAACCAATATTAATCTTCACAGAAAAGTA	4500
QY	4501	GTGAATTAACCCATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTACAAAGTTGAGGTGTG	4560
Db	4501	GTGAATTAACCCATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTACAAAGTTGAGGTGTG	4560
QY	4561	CAGATAGTTCTTACCAGTAAAAATTAAGAACACAGAGTGGAAAGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTTACCAGTAAAAATTAAGAACACAGAGTGGAAAGTCAATCCCTCTTAAT	4620
QY	4621	GCCCATCTTATGATGATAGGTGTACATGCACAGTGTGCTGGAGTCTTCAGAAATATAA	4680
Db	4621	GCCCATCTTATGATGATAGGTGTGTACATGCACAGTGTGCTGGAGTCTTCAGAAATATAA	4680
QY	4681	ACTTAACCATCTCAAGAGAGACCTCATTAAGGTTGTGATGTGAGAGCAACAGCTGGAG	4740
Db	4681	ACTTAACCATCTCAAGAGAGACCTCATTAAGGTTGTGATGTGAGAGCAACAGCTGGAG	4740
QY	4741	AGTCTGGGCCACAGACTTGTACGCGAAACATCTTACTTGGCAAGGCCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACAGACTTGTGTACGCGAAACATCTTACTTGGCAAGGCCAAGATCTAGAGGAA	4800
QY	4801	CCCCTTACCTGGAAATCTGGAATAGCCTCTTCTCTGATGACCTTGATCTATCCTCTTG	4860
Db	4801	CCCCTTACCTGGAAATCTGGAATAGCCTCTTCTCTGATGACCTTGATCTATCCTCTTG	4860
QY	4861	AAGACAGAGCCCAAGGTGACGCTCGTGTGGCAACATACATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAGACAGAGCCCAAGGTGACGCTCGTGTGGCAACATACATCTTCAACCTCTGCATTTGA	4920
QY	4921	AAGTCCCAATTAAGTAAGTTGACAGATCTGCCAGATCCAGATCTGCTGTATCTACTG	4980
Db	4921	AAGTCCCAATTAAGTAAGTTGACAGATCTGCCAGATCCAGATCTGCTGTATCTACTG	4980
QY	4981	ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTAGCAGGAGAGAACCAAAATTTGACAG	5040
Db	4981	ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTAGCAGGAGAGAACCAAAATTTGACAG	5040
QY	5041	CTTCAACAGAAAGGCTCAACAAAAGAAATCCATGATGTGTGTGCTGACCCCAAGAAAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAAGAAATCCATGATGTGTGTGCTGACCCCAAGAAAG	5100
QY	5101	AATTATAGCTGCTGTGTAAGTTGGCCAGAAAACACACATCATCTTAACTAATCTAATTA	5160

|||||  
Db 5101 AATTATGCTGGTACAAAGTTTGCAGAAAACCCACATCTTAACTAATTA 5160  
Oy 5161 CTGAAGAGACTACTCATGTGTTATGAAGACAGATGCTGAGTTGTGTGAAGCAGAC 5220  
Db 5161 CTGAAGAGACTACTCATGTGTTATGAAGACAGATGCTGAGTTGTGTGAAGCAGAC 5220  
Oy 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGTAGTTAGCTAATTTCCGGGTGACC 5280  
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGTAGTTAGCTAATTTCCGGGTGACC 5280  
Oy 5281 AGCTATTTAAAGAAAATGCTGAATGAGATGTTTGAATGAGAGGATGAG 5340  
Db 5281 AGCTATTTAAAGAAAATGCTGAATGAGATGTTTGAATGAGAGGATGAG 5340  
Oy 5341 TCATGGAAGAAACCAACCAAGTCCAAAGCAGACAGATCCAGAGAGAAAGATCT 5400  
Db 5341 TCATGGAAGAAACCAACCAAGTCCAAAGCAGACAGATCCAGAGAGAAAGATCT 5400  
Oy 5401 TCAGGGGCTAGAAATCTGTGTGATGAGGCTTACCAACATGCCAGATCACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTGTGATGAGGCTTACCAACATGCCAGATCACTGG 5460  
Oy 5461 AATGATGCTACAGTGTGTGCTCTGTGTGAGAGAGCTTTCATCATTCACCTTG 5520  
Db 5461 AATGATGCTACAGTGTGTGCTCTGTGTGAGAGAGCTTTCATCATTCACCTTG 5520  
Oy 5521 GCACAGAGTCTCCACCAATTTGTGTGTGAGCAGATGCTTGACAGAGACAAATGGCT 5580  
Db 5521 GCACAGAGTCTCCACCAATTTGTGTGTGAGCAGATGCTTGACAGAGACAAATGGCT 5580  
Oy 5581 TCCATGCAATTTGGGAGATGCTGTGAGGACACTGTGTGAGACCCGAGATGGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGCTGTGAGGACACTGTGTGAGACCCGAGATGGGTGTGACA 5640  
Oy 5641 GTGTAGACTCTACAGTGTGAGGACAGAGCTGACACTGATACCCAGATCCCGACACA 5700  
Db 5641 GTGTAGACTCTACAGTGTGAGGACAGAGCTGACACTGATACCCAGATCCCGACACA 5700  
Oy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 4  
LOCUS 176943 5914 bp DNA PAT 23-DEC-1997  
DEFINITION Sequence 1 from patent US 5693473.  
ACCESSION 176943  
NID 93013097  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5914)  
AUTHORS Shattuck-Eidens,D.M., Simard,J., Durocher,F., Eml,M. and Nakamura,Y.  
TITLE Linked breast and ovarian cancer susceptibility gene  
JOURNAL Patent: US 5693473-A 1 02-DEC-1997;  
FEATURES  
Location/Qualifiers  
1..5914  
BASE COUNT 2006 a 1156 c 1316 g 1436 t  
ORIGIN  
/organism="Unknown"

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGCTCGCTGAGACTTCTGTGAGCCCGCAGACGCTGTGGGTTTCTCAGATACTGGCC 60  
Db 1 AGCTCGCTGAGACTTCTGTGAGCCCGCAGACGCTGTGGGTTTCTCAGATACTGGCC 60

Oy 61 CTTGCGCTCAGAGGCGCTTACCCTCTGCTGTGGGTAAAGTTCAATTGAGACAGAGAAA 120  
Db 61 CTTGCGCTCAGAGGCGCTTACCCTCTGCTGTGGGTAAAGTTCAATTGAGACAGAGAAA 120  
Oy 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGATACAAAATGCTAATGCTATGACAGAAA 180  
Db 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGATACAAAATGCTAATGCTATGACAGAAA 180  
Oy 181 TCTTAGAGTCTCCATCTGCTGAGAGTGTATCAAGAGACCTGCTCCAGAAAGTGTACC 240  
Db 181 TCTTAGAGTCTCCATCTGCTGAGAGTGTATCAAGAGACCTGCTCCAGAAAGTGTACC 240  
Oy 241 ACATATTTTCAAAATTTTGCATGCTGAAACTTCTCAACAGAGAGAAAGGCTTCACT 300  
Db 241 ACATATTTTCAAAATTTTGCATGCTGAAACTTCTCAACAGAGAGAAAGGCTTCACT 300  
Oy 301 GTCTTTATGTAGAAATGATATACCAAAAGAGCTTACAAAGAAATACGATTTAGTC 360  
Db 301 GTCTTTATGTAGAAATGATATACCAAAAGAGCTTACAAAGAAATACGATTTAGTC 360  
Oy 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTCAGCTTGACAGGTTGGAGT 420  
Db 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTCAGCTTGACAGGTTGGAGT 420  
Oy 421 ATGCAAAACAGCTATTAATTTTGCAGAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
Db 421 ATGCAAAACAGCTATTAATTTTGCAGAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
Oy 481 AAGTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAGAGCTTCTACAGATG 540  
Db 481 AAGTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAGAGCTTCTACAGATG 540  
Oy 541 AACCCGAAAATCTCTCTGTCAGAGAAACAGCTCAGTGTCCAACTCTTAACCTTGGAA 600  
Db 541 AACCCGAAAATCTCTCTGTCAGAGAAACAGCTCAGTGTCCAACTCTTAACCTTGGAA 600  
Oy 601 CTGTGAAACTCTGAGAGACAAAGCAGGATACAACTTCAAAAAGAGCTGTCTACATG 660  
Db 601 CTGTGAAACTCTGAGAGACAAAGCAGGATACAACTTCAAAAAGAGCTGTCTACATG 660  
Oy 661 AATTGGATCTGATTTCTGTGAAGATACCGTTAATTAAGCACTTATGCAATGTTGGAG 720  
Db 661 AATTGGATCTGATTTCTGTGAAGATACCGTTAATTAAGCACTTATGCAATGTTGGAG 720  
Oy 721 ATCAAGATTTGTTCAAAATCACCCCTCAAGAGAACAGGATGAATCAATGTTGATCTG 780  
Db 721 ATCAAGATTTGTTCAAAATCACCCCTCAAGAGAACAGGATGAATCAATGTTGATCTG 780  
Oy 781 CAAAAAAGCTGCTGTGTGAATTTTCTGAGAGCGATGTAAACAATCTGAAATCATCAAC 840  
Db 781 CAAAAAAGCTGCTGTGTGAATTTTCTGAGAGCGATGTAAACAATCTGAAATCATCAAC 840  
Oy 841 CCAGTAAATGATTTGAAACACCACTGAGAGCGTGCAGTGAAGGATCCAGAAAAGT 900  
Db 841 CCAGTAAATGATTTGAAACACCACTGAGAGCGTGCAGTGAAGGATCCAGAAAAGT 900  
Oy 901 ATCAGGATGTTCTGTTTCAAACTGATGTGAGACCATGTCGCAAAATCTCATGCA 960  
Db 901 ATCAGGATGTTCTGTTTCAAACTGATGTGAGACCATGTCGCAAAATCTCATGCA 960  
Oy 961 GCTCATTTACAGATGAGAACAGCACTTATTAATCTCAATTAAGACAGAAATGATAGAAA 1020  
Db 961 GCTCATTTACAGATGAGAACAGCACTTATTAATCTCAATTAAGACAGAAATGATAGAAA 1020  
Oy 1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGGTTAGCAAGAGCCAAATATACGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGGTTAGCAAGAGCCAAATATACGAT 1080  
Oy 1081 GGGCTGGAAGTAAAGAAACATGATATGATAGCGGAGCTCCAGCAGAGAAAAAGGATG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGATATGATAGCGGAGCTCCAGCAGAGAAAAAGGATG 1140







Db 3301 TAGCTTCAGTGAAGAAACATTCAAGCAACCTAGTGAAGAAACAGAGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTATAGATTTAGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTTCTGGA 3420  
Db 3361 ATGCTATGCTTATAGATTTAGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTTCTGGA 3420  
QY 3421 GTATTTGTAAGCATCTCTAATAATAAAAAGCAAGAAATATAGAGAGTACTGACACTGTTA 3480  
Db 3421 GTATTTGTAAGCATCTCTAATAATAAAAAGCAAGAAATATAGAGAGTACTGACACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCATATCTGATTTGATTAAGTAAGCAAGCTATAGAGAGTACTGAC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTGATTAAGTAAGCAAGCTATAGAGAGTACTGAC 3540  
QY 3541 ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGATGAATTAAGG 3600  
Db 3541 ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGATGAATTAAGG 3600  
QY 3601 AAGTACTAGTTTGTCTGAGAAATGACATTAAGAAAGTTGCTGTTTTTACCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTCTGAGAAATGACATTAAGAAAGTTGCTGTTTTTACCAAAAGCG 3660  
QY 3661 TCCGAAAGAGAGAGCTTTCAGAGAGTCTAGAGCTTTCACCATACATTTGGCTCAGG 3720  
Db 3661 TCCGAAAGAGAGAGCTTTCAGAGAGTCTAGAGCTTTCACCATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCTAGAAAGAACTTATCTAGTGAAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCTAGAAAGAACTTATCTAGTGAAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTAAGTAACAAATTAACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTAAGTAACAAATTAACCTTCTCAGT 3840  
QY 3841 CTACTAGGCAATGACAGGCTTCTACAGAGTCTGCTTCTAGAAACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGGCAATGACAGGCTTCTACAGAGTCTGCTTCTAGAAACACAGAGAGATTTAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAAATGACTGAGTAACAGGTAATTTGGCCAAAGGCTATC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAAATGACTGAGTAACAGGTAATTTGGCCAAAGGCTATC 3960  
QY 3961 AGGAACATCACTTATGAGAGAAACAAATGTCTGCTAGTGTCTTCTACAGTGA 4020  
Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTCTGCTAGTGTCTTCTACAGTGA 4020  
QY 4021 GTGAATTTGAAGACTTGAAGTCAATTAACAAACCCAGAGATCTTCTTGAATGGTCTT 4080  
Db 4021 GTGAATTTGAAGACTTGAAGTCAATTAACAAACCCAGAGATCTTCTTGAATGGTCTT 4080  
QY 4081 CCAAAACAAATGAGGCAATCACTGTAAGAGCCAGGAGTTGGTCTGAGTACAGAGATTTGG 4140  
Db 4081 CCAAAACAAATGAGGCAATCACTGTAAGAGCCAGGAGTTGGTCTGAGTACAGAGATTTGG 4140  
QY 4141 TTTTCAGATTTGATGAAGAAAGAGAGGCTTGAAGAAATTAATCAAGAGCAAAACA 4200  
Db 4141 TTTTCAGATTTGATGAAGAAAGAGAGGCTTGAAGAAATTAATCAAGAGCAAAACA 4200  
QY 4201 TGGATTTCAAACTTATGAGTGAAGCAGACATCTGGGTGTGAGAGTGAACAACAGCTCTGAG 4260  
Db 4201 TGGATTTCAAACTTATGAGTGAAGCAGACATCTGGGTGTGAGAGTGAACAACAGCTCTGAG 4260  
QY 4261 ACTGCTTACAGGCTTCTCTCTAGAGTGAATTTTAAACATCAAGAGAGGATTAACATGC 4320  
Db 4261 ACTGCTTACAGGCTTCTCTCTAGAGTGAATTTTAAACATCAAGAGAGGATTAACATGC 4320  
QY 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTAGAGAGCTGTTAGAACGC 4380  
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTAGAGAGCTGTTAGAACGC 4380  
QY 4381 ATGGAGCCAGGCTTCTTAACAGCTACCTTCCATCAATTAAGTACTCTTCTGAGG 4440  
Db 4381 ATGGAGCCAGGCTTCTTAACAGCTACCTTCCATCAATTAAGTACTCTTCTGAGG 4440

QY 4441 ACCGCGAAATCCAGAAACAAAGCAGATCAAGAAAGCAGATTAATCTCAGAGAAAGTA 4500  
Db 4441 ACCGCGAAATCCAGAAACAAAGCAGATCAAGAAAGCAGATTAATCTCAGAGAAAGTA 4500  
QY 4501 GTGAATACCCTATTAAGCCAGATCCAGAGGCTTCTGCTGCAAGTTGAGGTGCTG 4560  
Db 4501 GTGAATACCCTATTAAGCCAGATCCAGAGGCTTCTGCTGCAAGTTGAGGTGCTG 4560  
QY 4561 CAGATAGTTCTTACAGATTAATAATTAAGAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTTACAGATTAATAATTAAGAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
QY 4621 GCCCATCTTATGATGATAGTGGTGTACATGCAACAGTCTCTGAGAGCTTCAAAATAGAA 4680  
Db 4621 GCCCATCTTATGATGATAGTGGTGTACATGCAACAGTCTCTGAGAGCTTCAAAATAGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGTGATGTGAGAGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGTGATGTGAGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGCTGGGCCACAGATTTGACGGAACATCTTACTTGCACAAAGCAGATCTAGAGGAA 4800  
Db 4741 AGCTGGGCCACAGATTTGACGGAACATCTTACTTGCACAAAGCAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTATGACCTGAAATCTGATCTTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTATGACCTGAAATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCCAGATGACGCTGCTGTTGGAACATTAACCTGCACTTGA 4920  
Db 4861 AAGACAGAGCCCCAGATGACGCTGCTGTTGGAACATTAACCTGCACTTGA 4920  
QY 4921 AAGTTCGCCAATTTGAAGTTGCAAGAAATCTGCCAGAGTCCAGCTGCTCATTAATCTAGT 4980  
Db 4921 AAGTTCGCCAATTTGAAGTTGCAAGAAATCTGCCAGAGTCCAGCTGCTCATTAATCTAGT 4980  
QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAACCAAGATTACAG 5040  
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAACCAAGATTACAG 5040  
QY 5041 CTTCAACGAAAGGGGTCAACAAAGAAATGTCATGGGTGGTCTGAGCTGAGCCCGAGAG 5100  
Db 5041 CTTCAACGAAAGGGGTCAACAAAGAAATGTCATGGGTGGTCTGAGCTGAGCCCGAGAG 5100  
QY 5101 AATTTATGCTGCTGTACAGATTTGCCAGAAACACCAATCACTTAATTAATTA 5160  
Db 5101 AATTTATGCTGCTGTACAGATTTGCCAGAAACACCAATCACTTAATTAATTA 5160  
QY 5161 CTGAAGAGACTACTCAATGTTGTATGAAAACAGATGCTGAGTTGTGTGAAAGGAGAC 5220  
Db 5161 CTGAAGAGACTACTCAATGTTGTATGAAAACAGATGCTGAGTTGTGTGAAAGGAGAC 5220  
QY 5221 TGAATATTTTCTTGAATTTGCCGAGAGAAATGGGATGATCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTTGAATTTGCCGAGAGAAATGGGATGATCTATTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATATTTTGAAGTCAAGAGGATGTGG 5340  
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATATTTTGAAGTCAAGAGGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCCAGAGGTCCAAGAGGAGCAGAGAAATCCAGAGACAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCCAGAGGTCCAAGAGGAGCAGAGAAATCCAGAGACAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATGTTGCTATGAGGGCTTCAACCAATGAGCCAGAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATGTTGCTATGAGGGCTTCAACCAATGAGCCAGAGATCAACTGG 5460  
QY 5461 AATGATGATGACAGCTGTGTGCTTGTGTGTGAGAGAGCTTTCATCATTCACCTTG 5520  
Db 5461 AATGATGATGACAGCTGTGTGCTTGTGTGTGAGAGAGCTTTCATCATTCACCTTG 5520



OY	1561	TAATTTAGAGACATTTGTTACTAGAGCCACAGATAATACAAAGACGTCCTCCACAATA	1623
Db	1561	TAATTTAGAGACATTTGTTACTAGAGCCACAGATAATACAAAGACGTCCTCCACAATA	1620
OY	1621	AATTAAGCGTAAAGAGACCTACATCAGGCCCTTCACTCTGAGATTTTATCAAGAA	1680
Db	1621	AATTAAGCGTAAAGAGACCTACATCAGGCCCTTCACTCTGAGATTTTATCAAGAA	1680
OY	1681	CAGATTGGCAGTTCAAAACACCTCCTAATATGATTAATTCAGGGAACTTACCAACGGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAACACCTCCTAATATGATTAATTCAGGGAACTTACCAACGGAGC	1740
OY	1741	AGAAATGCTCAAGTATGAATATTTACTAATATAGTGTGCTAGAGAAATAAAACAAGGTGAT	1800
Db	1741	AGAAATGCTCAAGTATGAATATTTACTAATATAGTGTGCTAGAGAAATAAAACAAGGTGAT	1800
OY	1801	CTATTAGAAATGAGAAAATCTTACCACTATAGATCACTCGAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTAGAAATGAGAAAATCTTACCACTATAGATCACTCGAAAAGAAATCTGCTTTCA	1860
OY	1861	AAACGAAGCTGAACCTATATAGAGACAGTATTAAGCAATATGGAACCTGGAATTAATATTC	1920
Db	1861	AAACGAAGCTGAACCTATATAGAGACAGTATTAAGCAATATGGAACCTGGAATTAATATTC	1920
OY	1921	ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGAGGAAGTCTTCCACGACATATTC	1980
Db	1921	ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGAGGAAGTCTTCCACGACATATTC	1980
OY	1981	ATGCGCTTGAACAGTATAGTACGTATGAGAAATCTAAGCCCACTAATTTGTAAGTATTCGAAA	2040
Db	1981	ATGCGCTTGAACAGTATAGTACGTATGAGAAATCTAAGCCCACTAATTTGTAAGTATTCGAAA	2040
OY	2041	TTGATAGTTGTTCTTACACAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGGCAGTCA	2100
Db	2041	TTGATAGTTGTTCTTACACAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGGCAGTCA	2100
OY	2101	GGCACAGCGAAAACCTACCACTCATGGAAGTAAAGAACTGCACTGAGGCCAAGAA	2160
Db	2101	GGCACAGCGAAAACCTACCACTCATGGAAGTAAAGAACTGCAACCTGCAACTGGAGCCAAAGAA	2160
OY	2161	GTACACAGCCAAATGAAACAGACAACTAAAAGACATGACAGATCTTCCACAGCTGA	2220
Db	2161	GTACACAGCCAAATGAAACAGACAACTAAAAGACATGACAGATCTTCCACAGCTGA	2220
OY	2221	AGTTAACAAATGCACCTGGTCTTTACTAAGTGTTCAAATACCAAGTAACTTAAAGAT	2280
Db	2221	AGTTAACAAATGCACCTGGTCTTTACTAAGTGTTCAAATACCAAGTAACTTAAAGAT	2280
OY	2281	TTGTCAATCTAGCCCTTCCAAAGGAAGAAAACAAGGAACCTAAGAAACAGTTAAATGT	2340
Db	2281	TTGTCAATCTAGCCCTTCCAAAGGAAGAAAACAAGGAACCTAAGAAACAGTTAAATGT	2340
OY	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTGCCAACTG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTGCCAACTG	2400
OY	2401	AAAGATCTTAGAGAGTACGAGTATTTCACTGGTACTGCTACTGATTATGCACTCAGG	2460
Db	2401	AAAGATCTTAGAGAGTACGAGTATTTCACTGGTACTGCTACTGATTATGCACTCAGG	2460
OY	2461	AAAGATATCTGTTACTGGAAGTATAGCACTTAGGGAAGGCAAAACGAACCAATTAAT	2520
Db	2461	AAAGATATCTGTTACTGGAAGTATAGCACTTAGGGAAGGCAAAACGAACCAATTAAT	2520
OY	2521	GTGTAGTCACTGTGCGACATTTGAAAACCCCAAGGAGCTAATTCAGTGTGTTCCAAAG	2580
Db	2521	GTGTAGTCACTGTGCGACATTTGAAAACCCCAAGGAGCTAATTCAGTGTGTTCCAAAG	2580
OY	2581	ATTAATTAAGAAATGACACAGAAAGGCTTTAAGTATCTATTGGGACATGAAGTTAACACAGTC	2640
Db	2581	ATTAATTAAGAAATGACACAGAAAGGCTTTAAGTATCTATTGGGACATGAAGTTAACACAGTC	2640

OY	2641	GGGAAACAGCATGGAATGGAAGAAAGTAAGTAAGTGTGCTGCTGCTTTGGCAAGTAATAC	2700
Db	2641	GGGAAACAGCATGGAATGGAAGAAAGTAAGTAAGTGTGCTGCTGCTTTGGCAAGTAATAC	2700
OY	2701	TCGAAGTTTCAAGCGCCAGTCATTTGCTGTGTTTTCAATCCAGGAAATGCAAGAGAG	2760
Db	2641	GGGAAACAGCATGGAATGGAAGAAAGTAAGTAAGTGTGCTGCTGCTTTGGCAAGTAATAC	2700
OY	2701	TCGAAGTTTCAAGCGCCAGTCATTTGCTGTGTTTTCAATCCAGGAAATGCAAGAGAG	2760
Db	2701	TCGAAGTTTCAAGCGCCAGTCATTTGCTGTGTTTTCAATCCAGGAAATGCAAGAGAG	2760
OY	2761	AATGGCAACATCTCTCGCCACCTGCGGGTCCTTAAGAAACCAAAAGTCCAAAAGTCACT	2820
Db	2761	AATGGCAACATCTCTCGCCACCTGCGGGTCCTTAAGAAACCAAAAGTCCAAAAGTCACT	2820
OY	2821	TTGAATGTGAACAAAGAGAAATATCAAGAAAGATGAGTAAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAGAAATATCAAGAAAGATGAGTAAATATCAAGCCTGTAC	2880
OY	2881	AGACAGTTAAATATCATCTGACGAGCCTTCCTGTGTTGTCAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAAATATCATCTGACGAGCCTTCCTGTGTTGTCAGAAAGATAGCCAGTTGATA	2940
OY	2941	ATGCCAAATAGTATATCAAAAGAGAGGCTCTAGTGTGTTGTCATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAAATAGTATATCAAAAGAGAGGCTCTAGTGTGTTGTCATCATCTCAGTTCAGAGCA	3000
OY	3001	ACGAAACTGGAATCTACTTCCAAATTAACATGAGCTTTTACAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGGAATCTACTTCCAAATTAACATGAGCTTTTACAAACCCATATCGTATAC	3060
OY	3061	CACACATTTTCCCATCAAGTCAATGCTATTTGTTAAACTAAATGTAAAGAAAATCGCTAGAG	3120
Db	3061	CACACATTTTCCCATCAAGTCAATGCTATTTGTTAAACTAAATGTAAAGAAAATCGCTAGAG	3120
OY	3121	AAAACTTTGAGGAACATTCATCTCACTGTCAAGAGAAATGGGAATGAGAACATTTCCA	3180
Db	3121	AAAACTTTGAGGAACATTCATCTCACTGTCAAGAGAAATGGGAATGAGAACATTTCCA	3180
OY	3181	GTAACAGGAGACAAATTAGCCGTAATTAACATTAGAAAAATGTTTTTAAAGAGCCACT	3240
Db	3181	GTAACAGGAGACAAATTAGCCGTAATTAACATTAGAAAAATGTTTTTAAAGAGCCACT	3240
OY	3241	CAACCAATATTTAAAGATGAGTGTTCACAGTCTAATGAGTGGGCTCCAGTATTAATGAA	3300
Db	3241	CAACCAATATTTAAAGATGAGTGTTCACAGTCTAATGAGTGGGCTCCAGTATTAATGAA	3300
OY	3301	TAGTTCACAGTATGAATCAATTCACAGAGACTAGTGAAGAAACAGAGGCCCAAAATTTGA	3360
Db	3301	TAGTTCACAGTATGAATCAATTCACAGAGACTAGTGAAGAAACAGAGGCCCAAAATTTGA	3360
OY	3361	ATGCTAGTCTAGATTGAGGGTTTGGCAACCTAGTCTATTAACAAAGTCTCTCTGGAA	3420
Db	3361	ATGCTAGTCTAGATTGAGGGTTTGGCAACCTAGTCTATTAACAAAGTCTCTCTGGAA	3420
OY	3421	GTAATTTGTAAAGCATCTGAAATATAAAAAGCAAGATATGAGAGTACTGACACTGTTA	3480
Db	3421	GTAATTTGTAAAGCATCTGAAATATAAAAAGCAAGATATGAGAGTACTGACACTGTTA	3480
OY	3481	ATTAAGATTTCTCTCCATATCTGATTTCCAGATTAACCTTAACAAAGCCTATGGGAAATATCT	3540
Db	3481	ATTAAGATTTCTCTCCATATCTGATTTCCAGATTAACCTTAACAAAGCCTATGGGAAATATCT	3540
OY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATATGATGGTGAATAAAG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATATGATGGTGAATAAAG	3600
OY	3601	AAGATCTAGTTTGTCTGAAATGACATTTAAGAAAGTCTGCTGTTTTTAAAGCAAAACGC	3660
Db	3601	AAGATCTAGTTTGTCTGAAATGACATTTAAGAAAGTCTGCTGTTTTTAAAGCAAAACGC	3660
OY	3661	TCCAGAAAGAGAGGCTTAGAGAGAGTCTTAAGCCCTTACCCATACAAATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGAGAGGCTTAGAGAGAGTCTTAAGCCCTTACCCATACAAATTTGGCTCAGG	3720
OY	3721	GTTTACCAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTGGAGAT	3780

|||||  
Db 3721 GTTCCGGAAGGGGCGCAAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTAGGATG 3780  
QY 3781 AAGAGCTCCCTGGTCCCAACACTTGTATTGGTAAAGTAAACAATATACCTCTCAGT 3840  
Db 3781 AAGAGCTCCCTGGTCCCAACACTTGTATTGGTAAAGTAAACAATATACCTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCCTGCTCAACGAGTCTGTCTAAGACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCCTGCTCAACGAGTCTGTCTAAGACACAGAGAGAAATTTAT 3900  
QY 3901 TATATTGAAGAAATAGCTTAATAGTCACTGACATCCAGGTAAATTTGGCAAGGACATCTC 3960  
Db 3901 TATATTGAAGAAATAGCTTAATAGTCACTGACATCCAGGTAAATTTGGCAAGGACATCTC 3960  
QY 3961 AGAACAATCACCCTTAGTGGAGGAAACAAATGTCTGACCTTTCTTCTTCTCAGAGTCA 4020  
Db 3961 AGAACAATCACCCTTAGTGGAGGAAACAAATGTCTGACCTTTCTTCTTCTCAGAGTCA 4020  
QY 4021 GTGAATTTGGAAGACTTGACCTGCAAAATCAAAACACCCAGAGATCTTTCTTGTGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACCTGCAAAATCAAAACACCCAGAGATCTTTCTTGTGTTCTT 4080  
QY 4081 CCAACAAGATAGGACATCAGTCTGAAGCCAGGAGTTGGTGTGAGTGAACAAGAAATGG 4140  
Db 4081 CCAACAAGATAGGACATCAGTCTGAAGCCAGGAGTTGGTGTGAGTGAACAAGAAATGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGAAAGGCGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGAAAGGCGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTCAAACTTAGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGCGCTCTGAG 4260  
Db 4201 TGGATTCAAACTTAGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGCGCTCTGAG 4260  
QY 4261 ACTGCTAGGGGCTTCTCTCTAGAGTGAATTTAAACCTCAGACAGAGGATACCATGC 4320  
Db 4261 ACTGCTAGGGGCTTCTCTCTAGAGTGAATTTAAACCTCAGACAGAGGATACCATGC 4320  
QY 4321 AACATACTGATTAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAAACAGC 4380  
Db 4321 AACATACTGATTAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAAACAGC 4380  
QY 4381 ATGGGAGCGAGCTTCTTAACAGCTACCTTCCATCAATAGGACTCTCTCCCTTGAAG 4440  
Db 4381 ATGGGAGCGAGCTTCTTAACAGCTACCTTCCATCAATAGGACTCTCTCCCTTGAAG 4440  
QY 4441 ACCGCGAAGATCCAGAACAAAGCAGATCAGAAAGAGATTAACCTTCACAGAAAGTA 4500  
Db 4441 ACCGCGAAGATCCAGAACAAAGCAGATCAGAAAGAGATTAACCTTCACAGAAAGTA 4500  
QY 4501 GTGAATACCTTATAGCCAGAGATCCAGAGGCTTTCTGTGACAGAGTTTGAAGTGTCTG 4560  
Db 4501 GTGAATACCTTATAGCCAGAGATCCAGAGGCTTTCTGTGACAGAGTTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTCTTACAGTAAATTAAGAACAGAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTCTTACAGTAAATTAAGAACAGAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
QY 4621 GCCCATATTAGATGATAGGAGTGAACATGACATGCTGCTGGAGAGCTTCAGAAATGAA 4680  
Db 4621 GCCCATATTAGATGATAGGAGTGAACATGACATGCTGCTGGAGAGCTTCAGAAATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGTGATGTGAGAGACAAACAGCTGGAAG 4740  
Db 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGTGATGTGAGAGACAAACAGCTGGAAG 4740  
QY 4741 AGTGTGGCCACAGAGATTTGACGGAACATCTTACTTGCCAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTGTGGCCACAGAGATTTGACGGAACATCTTACTTGCCAGGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACTGGAATCTGGAATCAGCCCTCTCTGATGAGACCTGAAATGATCTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGCCCTCTCTGATGAGACCTGAAATGATCTCTG 4860

Db 4801 CCCCTTACTGGAATCTGGAATCAGCCCTCTCTGATGAGACCTGAAATGATCTCTG 4860  
QY 4861 AAGACAGAGCCCGAGAGTCAAGCTGTGTGGCAACATACCATCTTCAACCTCTCATTA 4920  
Db 4861 AAGACAGAGCCCGAGAGTCAAGCTGTGTGGCAACATACCATCTTCAACCTCTCATTA 4920  
QY 4921 AAGTTCGCCAATTAAGTTGACAGATCTGCCAGAGTCCAGCTGTCTCATCTACTG 4980  
Db 4921 AAGTTCGCCAATTAAGTTGACAGATCTGCCAGAGTCCAGCTGTCTCATCTACTG 4980  
QY 4981 ATACTGGGTATTAAGCAATGGAAGAGTGTGACAGAGGAGAAACAGAAATGACAG 5040  
Db 4981 ATACTGGGTATTAAGCAATGGAAGAGTGTGACAGAGGAGAAACAGAAATGACAG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATAGTGTGTCTGGCTGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATAGTGTGTCTGGCTGACCCAGAG 5100  
QY 5101 AATTATGCTGCTGACAGATTTGCCAGAAACACACATCATCTTAATCTAATTA 5160  
Db 5101 AATTATGCTGCTGACAGATTTGCCAGAAACACACATCATCTTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTGTGAGAGGAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTGTGAGAGGAC 5220  
QY 5221 TGAATATTTTTCTAGAAATTCGCGAGAGAAATGGTAGTAACTATTTCTGGGTGACC 5280  
Db 5221 TGAATATTTTTCTAGAAATTCGCGAGAGAAATGGTAGTAACTATTTCTGGGTGACC 5280  
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGATGTGG 5340  
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGATGTGG 5340  
QY 5341 TCATGGAAGAAACCAAGAGTCCAAAGGAGAGCAAGAAATCCAGACAGAAAGATCT 5400  
Db 5341 TCATGGAAGAAACCAAGAGTCCAAAGGAGAGCAAGAAATCCAGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGTAGAAATGTTGCTATGAGGCGCTTCAACCAATGCCAGATCACTG 5460  
Db 5401 TCAGGGGGTAGAAATGTTGCTATGAGGCGCTTCAACCAATGCCAGATCACTG 5460  
QY 5461 AATGATGATGACAGCTGTGTGTCTCTGTGTGTAAGAGCTTATCATATCACCTTG 5520  
Db 5461 AATGATGATGACAGCTGTGTGTCTCTGTGTGTAAGAGCTTATCATATCACCTTG 5520  
QY 5521 GCACAGGTGCCACCAATGTGGTGTGACAGCAGATGCTGGACAGAGACAAATGGCT 5580  
Db 5521 GCACAGGTGCCACCAATGTGGTGTGACAGCAGATGCTGGACAGAGACAAATGGCT 5580  
QY 5581 TCCATGCAATTTGGCAGATGTGTGAGGACACCTGTGTGACCCGAGATGGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGCAGATGTGTGAGGACACCTGTGTGACCCGAGATGGGTGTGACA 5640  
QY 5641 GTGTAGCAGCTTACAGTGCAGAGAGCTGACACACTTATGATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCAGCTTACAGTGCAGAGAGCTGACACACTTATGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 6  
LOCUS 181034  
DEFINITION Sequence 1 from patent US 5710001.  
ACCESSION 181034  
NID 93209324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 5914)  
 AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,  
 Hartsman,K.D., Shattuck-Eidens,D.M., Tevligian,S.V., Wiseman,R.W.  
 and Futreal,P.Andrew.  
 TITLE 17q-linked breast and ovarian cancer susceptibility gene  
 JOURNAL Patent: US 5710001-A 1 20-JAN-1998;  
 FEATURES Location/Qualifiers  
 source 1..5914  
 /organism="unknown"  
 BASE COUNT 2006 a 1156 c 1316 g 1436 t  
 ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 AGCTCGTGAAGTCTCTGAGCCCGGACCGAGCTGTGGGTTCTCGATTAAGTGGCC 60
DB 1 AGCTCGTGAAGTCTCTGAGCCCGGACCGAGCTGTGGGTTCTCGATTAAGTGGCC 60
QY 61 CCTGCGTCAAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAGAGAA 120
DB 61 CCTGCGTCAAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAGAGAA 120
QY 121 TCGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGCTATTATGTCAGAAA 180
DB 121 TCGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGCTATTATGTCAGAAA 180
QY 181 TCTTAGAGTCCCATCTGTCTGAGTTGATCAAGAACTGTCCCAAGAGTGCAC 240
DB 181 TCTTAGAGTCCCATCTGTCTGAGTTGATCAAGAACTGTCCCAAGAGTGCAC 240
QY 241 ACATATTTTGCATATTTGCTGAACCTTCTCAACCAAGAGAGGCTTCAACAGT 300
DB 241 ACATATTTTGCATATTTGCTGAACCTTCTCAACCAAGAGAGGCTTCAACAGT 300
QY 301 GTCTTTATATGAAGATGATATACCAAGAGAGCTTCAAGAAATGCGAGATTAGTC 360
DB 301 GTCTTTATATGAAGATGATATACCAAGAGAGCTTCAAGAAATGCGAGATTAGTC 360
QY 361 AACTTGTGAAGAGCTATGTAATAATCATTTTGTCTTTCAGCTTGACAGAGTTGGAGT 420
DB 361 AACTTGTGAAGAGCTATGTAATAATCATTTTGTCTTTCAGCTTGACAGAGTTGGAGT 420
QY 421 ATGCAAAACAGCTATTAATTTGCAAAAAGAAATAACTCTCTGAACATCTAAAGATG 480
DB 421 ATGCAAAACAGCTATTAATTTGCAAAAAGAAATAACTCTCTGAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCTTCTTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCTTCTTACAGAGTG 540
QY 541 AACCCGAAATCCTTCTCTGAGAGAAACAGTCTCACTGTCCTCACTCTTAACTGGAA 600
DB 541 AACCCGAAATCCTTCTCTGAGAGAAACAGTCTCACTGTCCTCACTCTTAACTGGAA 600
QY 601 CTGTGAGAACTCTGAGAGCAAGAGCGGATACAACTCAAAAGAGCTGTGTACATG 660
DB 601 CTGTGAGAACTCTGAGAGCAAGAGCGGATACAACTCAAAAGAGCTGTGTACATG 660
QY 661 AATGGATCTGATTTCTTGAAGATACCGTTAATTAAGGCAACTTATGAGTGGAG 720
DB 661 AATGGATCTGATTTCTTGAAGATACCGTTAATTAAGGCAACTTATGAGTGGAG 720
QY 721 ATCAAGAAATGTAACAATACCCCTCAAGAACAGGAGTGAATGATGTTGATCTG 780
DB 721 ATCAAGAAATGTAACAATACCCCTCAAGAACAGGAGTGAATGATGTTGATCTG 780
QY 781 CAAAAAAGGCTGTTGTAATTTCTGAGAGCGATGTAAACAATATGAAATCATCAAC 840
DB 781 CAAAAAAGGCTGTTGTAATTTCTGAGAGCGATGTAAACAATATGAAATCATCAAC 840

```

```

QY 841 CCAATTAATGATTTTAACACCACTGAGAGCGTGCAGCTGAGAGCATCCGAAAGT 900
DB 841 CCAATTAATGATTTTAACACCACTGAGAGCGTGCAGCTGAGAGCATCCGAAAGT 900
QY 901 ATCAGGAGTCTGTTCTTCAAACTGCAATGGAGCATGTGACACAAATATCATGCCA 960
DB 901 ATCAGGAGTCTGTTCTTCAAACTGCAATGGAGCATGTGACACAAATATCATGCCA 960
QY 961 GCTCATTAAGCATGAGAGAGAGAGTTTATTAATCACTAATAAGACAGATGATGAAA 1020
DB 961 GCTCATTAAGCATGAGAGAGAGAGTTTATTAATCACTAATAAGATGATGAAA 1020
QY 1021 AAGCTGAATCTGTAATTAAGACCAAGAGCTGCTTGAAGAGACCAATTAAGAT 1080
DB 1021 AAGCTGAATCTGTAATTAAGACCAAGAGCTGCTTGAAGAGACCAATTAAGAT 1080
QY 1081 GGGCTGGAAGTAAGAAACATGTAATGATGGGGAGCTCCACAGAGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAGAAACATGTAATGATGGGGAGCTCCACAGAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAAGACGAAACTGCTATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAAGACGAAACTGCTATGCT 1200
QY 1201 CAGAGAACTCTAAGAGATCTGAAGATGTTCTTGATTAACACTTAATTAAGCATTCACA 1260
DB 1201 CAGAGAACTCTAAGAGATCTGAAGATGTTCTTGATTAACACTTAATTAAGCATTCACA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGATGTTAGTTTGTATGATCATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGATGTTAGTTTGTATGATCATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTAAGACGTTCTAAATGAGATGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTAAGACGTTCTAAATGAGATGATG 1380
QY 1381 AATATTTGCTTCTTCAAGAGAAATAGACTTACTGCGAGTACTCTCTGAGGCTTTAA 1440
DB 1381 AATATTTGCTTCTTCAAGAGAAATAGACTTACTGCGAGTACTCTCTGAGGCTTTAA 1440
QY 1441 TATTAATAAGTGAAGAGTCTCACTCCAAATCACTAAGAGATATGTAAGACAAATAT 1500
DB 1441 TATTAATAAGTGAAGAGTCTCACTCCAAATCACTAAGAGATATGTAAGACAAATAT 1500
QY 1501 TTGGGAAACCTATCGGAGAGAGAGGAGGCTCCCACTTAAGCCATGTAAGTGAATTC 1560
DB 1501 TTGGGAAACCTATCGGAGAGAGAGGAGGCTCCCACTTAAGCCATGTAAGTGAATTC 1560
QY 1561 TAATTAATGAGAGATTTGTTACTGAGCCACAGATTAATACAAAGAGCTCCCTCACAAATA 1620
DB 1561 TAATTAATGAGAGATTTGTTACTGAGCCACAGATTAATACAAAGAGCTCCCTCACAAATA 1620
QY 1621 AATTAAGAGCTTAAGAGAGAGCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680
DB 1621 AATTAAGAGCTTAAGAGAGAGCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAGACTTAACCAAGGAGC 1740
DB 1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAGACTTAACCAAGGAGC 1740
QY 1741 AGAATGGTCAAGTGAATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800
DB 1741 AGAATGGTCAAGTGAATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 CTATTCGAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGATCTGCTTTCA 1860
DB 1801 CTATTCGAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGATCTGCTTTCA 1860
QY 1861 AAACGAAAGCTGAACCTATTAAGCAGAGATTAAGCAATATGGAATCGAATTAATATCC 1920
DB 1861 AAACGAAAGCTGAACCTATTAAGCAGAGATTAAGCAATATGGAATCGAATTAATATCC 1920
QY 1921 ACAATTCAAAAAGCACTTAAGAAAGATAGGCTGAGAGGAAAGTCTTCTACAGGCAATATTC 1980

```

D	3001	ACGAACTGAGCTATTAATCTCCAAATAAATGAGACTTTTACAAAAACCATATGCTATAC	3068
Q	3061	CACCACTTTTCCATCAAGCTATTGTTAAATCTAATGTAGAAAAATCTGTAGAG	3120
D	3061	CACCACTTTTCCATCAAGCTATTGTTAAATCTAATGTAGAAAAATCTGTAGAG	3120
Q	3121	AAAACCTTGAGAACATTCAAATGCAACCGTAAGAAAGAAATGGAAATGGAACATTCGA	3180
D	3121	AAAACCTTGAGAACATTCAAATGCAACCGTAAGAAAGAAATGGAAATGGAACATTCGA	3180
Q	3181	GTACAGTAGACAAATTAGCCGTAAATACATTAGAAAAATGTTTTTAAGAAGCAGCT	3240
D	3181	GTACAGTAGACAAATTAGCCGTAAATACATTAGAAAAATGTTTTTAAGAAGCAGCT	3240
Q	3241	CAAGCAATATTAAATGAATAGGTTCCAGTACTAATGAGTGCGCTCAGTATTAAAGAA	3300
D	3241	CAAGCAATATTAAATGAATAGGTTCCAGTACTAATGAGTGCGCTCAGTATTAAAGAA	3300
Q	3301	TAGGTTCCAGTAGTGAATAACATTCAGCAGACTAGGTGAAACAGAGGCCAAATTGA	3360
D	3301	TAGGTTCCAGTAGTGAATAACATTCAGCAGACTAGGTGAAACAGAGGCCAAATTGA	3360
Q	3361	ATGCAATCTTAAGATTAGGGGTTTTGCACCTGAGGCTATATAACAAGTCTCTCTGGA	3420
D	3361	ATGCAATCTTAAGATTAGGGGTTTTGCACCTGAGGCTATATAACAAGTCTCTCTGGA	3420
Q	3421	GTAATTGTAACTATCCGAAATATAAAGCAGAAATATGAATAGTTCAGACTGTTA	3480
D	3421	GTAATTGTAACTATCCGAAATATAAAGCAGAAATATGAATAGTTCAGACTGTTA	3480
Q	3481	ATACAGATTTCTTCATATCTGATTTCAATTAATTTAGAACGCTATGGAGTACTC	3540
D	3481	ATACAGATTTCTTCATATCTGATTTCAATTAATTTAGAACGCTATGGAGTACTC	3540
Q	3541	ATGCACTCAGGCTTTGTTCTGAGAACCCGATGACCTGTATCATATGTTGAATAAAG	3600
D	3541	ATGCACTCAGGCTTTGTTCTGAGAACCCGATGACCTGTATCATATGTTGAATAAAG	3600
Q	3601	AAGATACAGTTTGTGCTGAATAATGACATTAGGAAGTTCTGCTGTTTATAGCAAAACG	3660
D	3601	AAGATACAGTTTGTGCTGAATAATGACATTAGGAAGTTCTGCTGTTTATAGCAAAACG	3660
Q	3661	TCCAGAAAGAGAGCTTAGCAGAGAGTCCTAGCCCTTTCACCATACACATTTGGCTCAG	3720
D	3661	TCCAGAAAGAGAGCTTAGCAGAGAGTCCTAGCCCTTTCACCATACACATTTGGCTCAG	3720
Q	3721	GTTACCGAAGGGGCCAAGAAATTAGAGTCCCAAGAAAGAACTTACTAGTAGAGT	3780
D	3721	GTTACCGAAGGGGCCAAGAAATTAGAGTCCCAAGAAAGAACTTACTAGTAGAGT	3780
Q	3781	AAGAGCTCCCTGTTCAACACCTGTATTTGTTAAATGAACAATATACCTCTCAGT	3840
D	3781	AAGAGCTCCCTGTTCAACACCTGTATTTGTTAAATGAACAATATACCTCTCAGT	3840
Q	3841	CTACTAGCATAGCAGCCGTTGCTACGAGTGTGCTCTAGAAACACAGAGGAGATTAT	3900
D	3841	CTACTAGCATAGCAGCCGTTGCTACGAGTGTGCTCTAGAAACACAGAGGAGATTAT	3900
Q	3901	TATCATTTGAAGATAGCTTAATGACTGCAGTACCAGGTAATATTGGCAAGGATCTC	3960
D	3901	TATCATTTGAAGATAGCTTAATGACTGCAGTACCAGGTAATATTGGCAAGGATCTC	3960
Q	3961	AGGAACATCACCTTAGTGAGAGAAACAAATGTTCTGCTGCTTTCTTCACAGTCA	4020
D	3961	AGGAACATCACCTTAGTGAGAGAAACAAATGTTCTGCTGCTTTCTTCACAGTCA	4020
Q	4021	GTAATTTGAAGACTTACTCTGCAAAATACAAACCCAGAGTCTTCTGATTTGGTTT	4080
D	4021	GTAATTTGAAGACTTACTCTGCAAAATACAAACCCAGAGTCTTCTGATTTGGTTT	4080
Q	4081	CCAAACAAATGAGGCATCACTGTAAGAGCCAGGAGTTGCTGTAGTAGACAAGAAATGG	4140
D	4081	CCAAACAAATGAGGCATCACTGTAAGAGCCAGGAGTTGCTGTAGTAGACAAGAAATGG	4140



QY 4141 TTTCAGATGATGAAGAAAGAGAACGGCTTGGAAAGAAATATCAAGAGCAAGCA 4200  
 DB 4141 TTTCAGATGATGAAGAAAGAGAACGGCTTGGAAAGAAATATCAAGAGCAAGCA 4200  
 QY 4201 TGGATTAATTTGAGTGAAGAGCATCTGGGTGAGAGTGAACCAAGCGCTCTGAAG 4260  
 DB 4201 TGGATTAATTTGAGTGAAGAGCATCTGGGTGAGAGTGAACCAAGCGCTCTGAAG 4260  
 QY 4261 ACTGCTGAGGCTATCTCTGAGAGTGAATTTAAACCACTGAGAGAGGATACCATGC 4320  
 DB 4261 ACTGCTGAGGCTATCTCTGAGAGTGAATTTAAACCACTGAGAGAGGATACCATGC 4320  
 QY 4321 AACCTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTGATTAAGAGAGC 4380  
 DB 4321 AACCTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTGATTAAGAGAGC 4380  
 QY 4381 ATGGAGAGCAGCTTCTTAACAGCTACCTCCATCATAGTGAATCTTCTGCTTGAAG 4440  
 DB 4381 ATGGAGAGCAGCTTCTTAACAGCTACCTCCATCATAGTGAATCTTCTGCTTGAAG 4440  
 QY 4441 ACCTGCAAAATCCAGAAACAGACATCAGAAAAGAGATTAATTCACAGAAAAGTA 4500  
 DB 4441 ACCTGCAAAATCCAGAAACAGACATCAGAAAAGAGATTAATTCACAGAAAAGTA 4500  
 QY 4501 GTGATACCTCTATTAAGCCAGATCCAGAAAGCTTCTGCTGACAAAGTTGAGGTCTG 4560  
 DB 4501 GTGATACCTCTATTAAGCCAGATCCAGAAAGCTTCTGCTGACAAAGTTGAGGTCTG 4560  
 QY 4561 CAGATAGTTTACAGATTAATAAGAAACAGAGAGTGAAGAGTCACTCCCTTTAAAT 4620  
 DB 4561 CAGATAGTTTACAGATTAATAAGAAACAGAGAGTGAAGAGTCACTCCCTTTAAAT 4620  
 QY 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
 DB 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
 QY 4681 ACTGATCATTAAG 4740  
 DB 4681 ACTGATCATTAAG 4740  
 QY 4741 AGTCTGGGCCCACAGATTTGAGAGAAACATCTTACTTCCAAAGCAAGATCTAGAGGA 4800  
 DB 4741 AGTCTGGGCCCACAGATTTGAGAGAAACATCTTACTTCCAAAGCAAGATCTAGAGGA 4800  
 QY 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTCTGATGATGATGATGATGATGATG 4860  
 DB 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTCTGATGATGATGATGATGATGATG 4860  
 QY 4861 AAGACAGAGCCGAG 4920  
 DB 4861 AAGACAGAGCCGAG 4920  
 QY 4921 AAGTTCCTCAATTAAGATTTGAGAGAAACATCTTACTTCCAAAGCAAGATCTAGAGGA 4980  
 DB 4921 AAGTTCCTCAATTAAGATTTGAGAGAAACATCTTACTTCCAAAGCAAGATCTAGAGGA 4980  
 QY 4981 AATCTGCTGGTATTAATGCAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040  
 DB 4981 AATCTGCTGGTATTAATGCAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040  
 QY 5041 CTTCACAG 5100  
 DB 5041 CTTCACAG 5100  
 QY 5101 AATTTATGCTGCTGATGAAGTTTCCAGAGAAACACACATCACTTAATTAATTAATTA 5160  
 DB 5101 AATTTATGCTGCTGATGAAGTTTCCAGAGAAACACACATCACTTAATTAATTAATTA 5160  
 QY 5161 CTGAGAGAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
 DB 5161 CTGAGAGAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220

QY 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTATTTCTGGGTGACC 5280  
 DB 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTATTTCTGGGTGACC 5280  
 QY 5281 AGCTATTAAGAAAGAAAGAAATGCTGAATGAGATTTTGAAGTGAAGAGATGAG 5340  
 DB 5281 AGCTATTAAGAAAGAAAGAAATGCTGAATGAGATTTTGAAGTGAAGAGATGAG 5340  
 QY 5341 TCAATGAAGAAACCCAGAGTCCAAAGCAGAGAGAGAGAGAGAGAGAGAGAGATCT 5400  
 DB 5341 TCAATGAAGAAACCCAGAGTCCAAAGCAGAGAGAGAGAGAGAGAGAGAGAGATCT 5400  
 QY 5401 TCAGGGGCTAGAAATCTGTTGATGAGGCTTCTGACCAACATGCCCCAGATCAACTGG 5460  
 DB 5401 TCAGGGGCTAGAAATCTGTTGATGAGGCTTCTGACCAACATGCCCCAGATCAACTGG 5460  
 QY 5461 AATGATGATGAGAGTGTGCTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 5520  
 DB 5461 AATGATGATGAGAGTGTGCTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 5520  
 QY 5521 GCACAGGTGTCACCCCAATTTGTTGTCAGCCAGATGCTTGACAGAGAGAGAGAGAGAG 5580  
 DB 5521 GCACAGGTGTCACCCCAATTTGTTGTCAGCCAGATGCTTGACAGAGAGAGAGAGAGAG 5580  
 QY 5581 TCCATGCAATTTGGGCAATGTTGAGAGCAGCTGTGATGAGAGAGAGAGAGAGAGAGAG 5640  
 DB 5581 TCCATGCAATTTGGGCAATGTTGAGAGCAGCTGTGATGAGAGAGAGAGAGAGAGAGAG 5640  
 QY 5641 GTGTAGCACTTACAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
 DB 5641 GTGTAGCACTTACAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711

## RESULT 7

HSD14680 5711 bp mRNA PRI 05-AUG-1995  
 LOCUS Human breast and ovarian cancer susceptibility (BRCA1) mRNA,  
 DEFINITION complete cds.  
 ACCESSION U14680  
 NID g555931  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

## REFERENCE

AUTHORS  
 1 (bases 1 to 5711)  
 Miki Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harsman K., Tavtigian S., Liu Q., Cochran C., Bennett L.M., Ding W., Bell R., Rosenthal J., Hussey C., Tran T., McClure M., Frye C., Hattler T., Phelps R., Haugen-Strano A., Katcher H., Yakumo K., Gholami Z., Shaffer D., Stone S., Bayer S., Wray C., Bogden R., Dayananth P., Ward J., Tonin P., Narod S., Bristow P.K., Norris F.H., Helvering L., Morrison P., Rostek P., Lai M., Barrett J.C., Lewy S., Neuhausen S., Cannon-Albright L., Goldgar D., Wiseman R., Kamb A. and Skolnick M.H.  
 A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1

JOURNAL Science 266 (5182), 66-71 (1994)  
 MEDLINE 9502896  
 REFERENCE 2 (bases 1 to 5711)  
 AUTHORS Skolnick M.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA

## FEATURES

1. 5711  
 /organism="Homo sapiens"  
 /note="For sequence of alternatively spliced exon 4, see



GenBank Accession Number U15595"  
/db\_xref="taxon:9606"  
/chromosome="17"  
/map="17q21; spans D17S855"  
1..119  
1..100  
/number=1  
101..199  
/number=2  
120..5711  
/gene="BRCA1"  
120..5711  
/gene="BRCA1"  
/note="Influences susceptibility to breast and ovarian cancer"  
/codon\_start=1  
/db\_xref="PID:9555932"  
/translation="MDLSALRVEVQVYINAMOKILIECPICLETIKRPVSNKCDHIC  
KFCMLKILNOKGSPGOCPLKNDITKRSIQSTSPFSQVYELLKTIICAFQDPTCLEA  
NSYMPAKKENSPPHLKDEVSITQSGMGRNKAHLQSEPEPNSLOETSLVSQVLSNG  
TVRLTRKQRIQPKTSYVIELGSDSSSDYTNKATYCSVGQELQITPQTRNLSL  
DSAKACAESESDVNTNENHOPSNNDLITERKPAERHPEKYOGSVSNLHVPCT  
NTHASIQHENSLLTKDRNAVKEAFCNKSQGLARSOHNMAGSKETCNDRRP  
STEKVDLADPLCEKEMNOKLPCSENPRTDTEPMITLNSIQKVENESDEL  
LGSDSHDGESENAKAVADVYNDEYSGSEKIDILADPHALICKSEVHAK  
SVESNIEDKIRGKTKRKASLPNLSHTTENTITATFTEPOTIOERPLINKRRRP  
TSGLHPEDFIKADLAVOKTEPMINOGTQEQVANNITNSGHEKTKDSIQNEK  
NPNDIESLEKSAKTAEPISSEISINNELELNHNSKAPKKNLRKSRHIALE  
LVVSRNLSPNCTELQIDSCSSEIKKKKNQMPVRSNRLQIMEKEPATGAKKN  
KPNQTSKRHSDTEPELKLINAPGSPFKCSNTSELKEFVPSLPREKKEKLTIVY  
SNMADPKDMLSGEVLQTPRSVSSSISVPTGDTGQPSISLFEVSTGKAKTP  
NKCYSQCAEPENPGILHGCSDNRNDTEGKTYLGHVYNSKETSIMESSELDQK  
LQNTFKVSKRQSFAPSNPGNAEECAFEASHSLKQSPKVTCEQKENGKME  
SNIPVQTVNTAGPVPVQGDKNVDNAKCSIKGSRFCLSOPRGNETGLITPNKG  
LQMPYRIPPLPIKSEVTKCKKNLLENEEESMSPEREMENIPSTVTSRNN  
IRENVFEASSNINEGSSNINEGSSNINEGSSNINEGSSNINEGSSNINEGSSN  
SEDCSGSSOSDILITTOORDIMONHLIKIOEMLEAVLEOHSGPASAQSPSTISDS  
SALDELNPNETSEKAVITQSSEYVPSONPGLSADKFEVADSSTSKNKPQVE  
RSFSKPSLDDRTYHSCSGSLQNRNTPSEBELIKVADVEQQLSESPDLTETSL  
LPRLDGETPLEGISLFSDDPSDPSDPAARAGNIPSSISLAKVQLVAAS  
AQSPAATHTDTIAGYNAMEESVSREKPELITSTERYKRMGMVSGLPPEFMTLYF  
ARKHILITLNTIETTHVYAKTDAEFVCERTLTFFGIAGKVVVSYFVWTSIKER  
KMLNEHPEVGVGVNGRHHGPKRARSODRKLPRLGELTCYGPFTNMPDQLEMYV  
OLGASVYKELSFSTIGVHPPIYVQPDATENDNGHAIQMCENAVYVIREVLDVY  
ALYCOEDELITLIPQIPHSY"  
200..253  
/gene="BRCA1"  
/number=3  
254..331  
/gene="BRCA1"  
/number=5  
332..420  
/gene="BRCA1"  
/number=6  
421..560  
/gene="BRCA1"  
/number=7  
561..665  
/gene="BRCA1"  
/number=8  
666..712  
/gene="BRCA1"  
/number=9  
713..788  
/gene="BRCA1"  
/number=10  
789..4215  
/gene="BRCA1"

	Query Match	100.0%; Score 5709.4; DB 10; Length 5711;
QY	1 AGCTGCGTGAACACTTCTCGACCCCGACACAGGCTGTGGGTTTCTCAGATPACTGGGCC	60
Db	1 AGCTGCGTGAACACTTCTCGACCCCGACACAGGCTGTGGGTTTCTCAGATPACTGGGCC	60
QY	61 CCGGCGCTCAGAGAGCCCTTCAACCTCTGCTGGGTAAGTTGAGACAGAAAGAA	120
Db	61 CCGGCGCTCAGAGAGCCCTTCAACCTCTGCTGGGTAAGTTGAGACAGAAAGAA	120
QY	121 TGGATTTATCTGCTCTCGCGTTGAGAGATACAAATGTCTTATATGCTATGCGAGAAA	180
Db	121 TGGATTTATCTGCTCTCGCGTTGAGAGATACAAATGTCTTATATGCTATGCGAGAAA	180
QY	181 TGGATTTATCTGCTCTCGCGTTGAGAGATACAAATGTCTTATATGCTATGCGAGAAA	240
Db	181 TGGATTTATCTGCTCTCGCGTTGAGAGATACAAATGTCTTATATGCTATGCGAGAAA	240
QY	241 ACATATTTTGAATTTTGCATGCTGGAACCTTCAACAGAGAAAGGCTTCACAGT	300
Db	241 ACATATTTTGAATTTTGCATGCTGGAACCTTCAACAGAGAAAGGCTTCACAGT	300
QY	301 GTCCCTTATGTAGAGATGATATTAACCAAAAGAGACCTACAGAAAGTACGAGATTAGTC	360
Db	301 GTCCCTTATGTAGAGATGATATTAACCAAAAGAGACCTACAGAAAGTACGAGATTAGTC	360
QY	361 AACTTGTTGAAGACCTATTCGAAATCATTTGTGCTTTACGCTTGACACAGGTTTGAGT	420

BASE COUNT 1956 a 1099 c 1274 g 1382 t

ORIGIN

Query Match 100.0%; Score 5709.4; DB 10; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Db 361 AACTGTGGAAGACTATGAAAAATCATTTGTGCTTTACACTTGACACAGTTGGAGT 420
QY 421 ATGCAACAGCTATTAATTTGCAAAAAAGAAATTAAGTCTCTGATCATCTAAAAAGATG 480
Db 421 ATGCAACAGCTATTAATTTGCAAAAAAGAAATTAAGTCTCTGATCATCTAAAAAGATG 480
QY 481 AAGTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGAGTG 540
Db 481 AAGTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGAGTG 540
QY 541 AACCCGAAATCCCTCTCTGAGGAAACCACTCAAGTGTCCAACTCCTAACTTGGAA 600
Db 541 AACCCGAAATCCCTCTCTGAGGAAACCACTCAAGTGTCCAACTCCTAACTTGGAA 600
QY 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATACAACCTCAAAAGAGCTGTGCTACATG 660
Db 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATACAACCTCAAAAGAGCTGTGCTACATG 660
QY 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAGTGGGAG 720
Db 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAGTGGGAG 720
QY 721 ATGAGAAATGTTCAATATCCCTCAAGGAAACGAGGATGAATCAGTTGATCTG 780
Db 721 ATGAGAAATGTTCAATATCCCTCAAGGAAACGAGGATGAATCAGTTGATCTG 780
QY 781 CAAAAAGGCTGCTTGTGAATTTCTGAGAGGATGTAAACAATCTGATCATCATCAAC 840
Db 781 CAAAAAGGCTGCTGTTGAATTTCTGAGAGGATGTAAACAATCTGATCATCATCAAC 840
QY 841 CCAATTAATTAATGATTTGAACACCACTGAAAGCGTGCAGCTGAGAGCATCCAGAAAAGT 900
Db 841 CCAATTAATTAATGATTTGAACACCACTGAAAGCGTGCAGCTGAGAGCATCCAGAAAAGT 900
QY 901 ATGAGGATGCTGTTCAAACTTGATGAGGCACTGAGGCACTGAGGCACTGATGCA 960
Db 901 ATGAGGATGCTGTTCAAACTTGATGAGGCACTGAGGCACTGAGGCACTGATGCA 960
QY 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTACTTAAAGACAGATGATGAAA 1020
Db 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTACTTAAAGACAGATGATGAAA 1020
QY 1021 AGGCTGAATCTGTAATTAATAAGCAACAGCTGCTTACGAAGAGCCACATTAACAGAT 1080
Db 1021 AGGCTGAATCTGTAATTAATAAGCAACAGCTGCTTACGAAGAGCCACATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGACTCCAGCAGCAAGAAAAAGTAG 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGACTCCAGCAGCAAGAAAAAGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAGAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAGAACTGCCATGCT 1200
QY 1201 CAGAGATCTTAAGATATCTGAAAGATGTTAGTGTGATTAATAGCAGATTCGA 1260
Db 1201 CAGAGATCTTAAGATATCTGAAAGATGTTAGTGTGATTAATAGCAGATTCGA 1260
QY 1261 AAGTTAATGAGTGGTTTCCGAGAGTGAATGTTAGTGTGATTAATAGCAGATTCGA 1320
Db 1261 AAGTTAATGAGTGGTTTCCGAGAGTGAATGTTAGTGTGATTAATAGCAGATTCGA 1320
QY 1321 GGGAGTCTGAATCAAAATGCAAAAGTAGCTGATGATGAGAGTTCTTAATAGGATAGT 1380
Db 1321 GGGAGTCTGAATCAAAATGCAAAAGTAGCTGATGATGAGAGTTCTTAATAGGATAGT 1380
QY 1381 AATATTTCTGTTCTTCCAGAGAAATAGACTTACTGCGCAGTGAATCTTAA 1440
Db 1381 AATATTTCTGTTCTTCCAGAGAAATAGACTTACTGCGCAGTGAATCTTAA 1440
QY 1441 TATGTAAAAGTGAAGAGTCACTCCAAATCAGTAGAGATTAATGAACAAAATAT 1500
Db 1441 TATGTAAAAGTGAAGAGTCACTCCAAATCAGTAGAGATTAATGAACAAAATAT 1500

Db 1501 TTGGGAAAACCTATCGGAGAGGCAAGCCCTCCCAACTTAAGCCTGTAACGTAATAATC 1560
QY 1501 TTGGGAAAACCTATCGGAGAGGCAAGCCCTCCCAACTTAAGCCTGTAACGTAATAATC 1560
Db 1501 TTGGGAAAACCTATCGGAGAGGCAAGCCCTCCCAACTTAAGCCTGTAACGTAATAATC 1560
QY 1561 TAATTTATGAGACATTTGTTACTGAGCCACAGATTAATACAGAGCTCCCTACAAATA 1620
Db 1561 TAATTTATGAGACATTTGTTACTGAGCCACAGATTAATACAGAGCTCCCTACAAATA 1620
QY 1621 AATTAAGCCGTAAGAGAGCTCATCAGGCTTCATCCCTGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGCCGTAAGAGAGAGCTCATCAGGCTTCATCCCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAGTAACCAAGGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAGTAACCAAGGAGC 1740
QY 1741 AGAATGGTCAAGTGTGATTAATTAATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 AGAATGGTCAAGTGTGATTAATTAATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 CTATTCAGAAATGAGAAATCTTAACCAATAGATCAGTCAAGAAAGATGCTTTCA 1860
Db 1801 CTATTCAGAAATGAGAAATCTTAACCAATAGATCAGTCAAGAAAGATGCTTTCA 1860
QY 1861 AAGGAAAGCTGAACTTAATAGCAGAGTAAAGCAATATGAACTGAAATTAATATATC 1920
Db 1861 AAGGAAAGCTGAACTTAATAGCAGAGTAAAGCAATATGAACTGAAATTAATATATC 1920
QY 1921 ACAATTTAAAAAGCCTTAATAAAGATTAAGCTGAGAGGAAAGTCTTACAGGCAATATC 1980
Db 1921 ACAATTTAAAAAGCCTTAATAAAGATTAAGCTGAGAGGAAAGTCTTACAGGCAATATC 1980
QY 1981 ATGCGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Db 1981 ATGCGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
QY 2041 TTGATAGTTGTTTACAGAGTGAAGAGATTAAGAAAGAAAAAGTACAAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTTGTTTACAGAGTGAAGAGATTAAGAAAGAAAAAGTACAAACCAATGCCAGTCA 2100
QY 2101 GGCACACAGAAACCTTAACATCATGGAAGGTAAGAACTGCACTGAGCCAGAGAGA 2160
Db 2101 GGCACACAGAAACCTTAACATCATGGAAGGTAAGAACTGCACTGAGCCAGAGAGA 2160
QY 2161 GTAACAAGCCAAATGAACACAGATTAAGAAAGATGATGATGATGATGATGATGATGATG 2220
Db 2161 GTAACAAGCCAAATGAACACAGATTAAGAAAGATGATGATGATGATGATGATGATGATG 2220
QY 2221 AGTTAACAAATGCACTGCTGTTTACTAAGTGTTCAAATACCACTGAACTTAAGAT 2280
Db 2221 AGTTAACAAATGCACTGCTGTTTACTAAGTGTTCAAATACCACTGAACTTAAGAT 2280
QY 2281 TTGTCATCTCTAGCTTCCCAAGAGAAAGAAAGAAAGAAAGAAAGAAAGTAAAGT 2340
Db 2281 TTGTCATCTCTAGCTTCCCAAGAGAAAGAAAGAAAGAAAGAAAGAAAGTAAAGT 2340
QY 2341 CTAATTAATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAAACTG 2400
Db 2341 CTAATTAATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAAACTG 2400
QY 2401 AAGATCTGTAAGAGATGAGAGATTTCAATGTTGATCTGATCTGATTAATGACAGT 2460
Db 2401 AAGATCTGTAAGAGATGAGAGATTTCAATGTTGATCTGATCTGATTAATGACAGT 2460
QY 2461 AAGATCTGTAAGAGATGAGAGATTTCAATGTTGATCTGATCTGATTAATGACAGT 2520
Db 2461 AAGATCTGTAAGAGATGAGAGATTTCAATGTTGATCTGATCTGATTAATGACAGT 2520
QY 2521 GTGAGATCAGTGTGAGAGATTTGAAAGCCCAAGGAGTAAATGATGATGATGATGATG 2580
Db 2521 GTGAGATCAGTGTGAGAGATTTGAAAGCCCAAGGAGTAAATGATGATGATGATGATG 2580
```

QY	2581	ATATAGAAATGACACGAGAGCGCTTTTAAGTATCCATTTGGGAATGAAGTTAACCAAGCTC	2640
Db	2581	ATAATAGAAATGACACGAGAGCGCTTTTAAGTATCCATTTGGGAATGAAGTTAACCAAGCTC	2640
QY	2641	GGGAAACAGCATGTGAATGGAAGAAAGTGAACCTTATCTCAGTATTGGCGAATACAT	2700
Db	2641	GGGAAACAGCATGTGAATGGAAGAAAGTGAACCTTATCTCAGTATTGGCGAATACAT	2700
QY	2701	TCGAGTTTCAAGCGCCAGTCAATTTGCTGTGTTTTCAATCCAGGAAATCGAGAGAGG	2760
Db	2701	TCGAGTTTCAAGCGCCAGTCAATTTGCTGTGTTTTCAATCCAGGAAATCGAGAGAGG	2760
QY	2761	AATGCGAACATCTCTCGGCCACTCTGGGGCTTTAAGAAACAAAGTCCAAAAGCACTT	2820
Db	2761	AATGCGAACATCTCTCGGCCACTCTGGGGCTTTAAGAAACAAAGTCCAAAAGCACTT	2820
QY	2821	TTGATGTGAACAAAGAGAAAGAAATCAAGAAAGATGACTAATATCAAGCCTGTAC	2880
Db	2821	TTGATGTGAACAAAGAGAGAAAGAAATCAAGAAAGATGACTAATATCAAGCCTGTAC	2880
QY	2881	AGACAGTTAATATCACCTCGAGCGCTTTCCTGTGGTGGTGAAGAAATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACCTCGAGCGCTTTCCTGTGGTGGTGAAGAAATAGCCAGTTGATA	2940
QY	2941	ATGCCAATGTAGTATCAAGAGAGCGCTAGTTTTGTCTATCATCTCAGTTCAGAGACA	3000
Db	2941	ATGCCAATGTAGTATCAAGAGAGCGCTAGTTTTGTCTATCATCTCAGTTCAGAGACA	3000
QY	3001	ACGAACTGCATCTATTCCTCCAAATPAACATGAGACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAACTGCATCTATTCCTCCAAATPAACATGAGACTTTTACAAAACCCATATCGTATAC	3060
QY	3061	CACACATTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTAGAAAAATCGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTAGAAAAATCGCTAGAGG	3120
QY	3121	AAAACTTGAAGAACATTTCAATGTCACTGAAAGAGAAATGGAAATGAGAACATTTCCA	3180
Db	3121	AAAACTTGAAGAACATTTCAATGTCACTGAAAGAGAAATGGAAATGAGAACATTTCCA	3180
QY	3181	GTACAGTGACACAAATTAGGCCGTTATPAACATTAGAAAAATTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGACACAAATTAGGCCGTTATPAACATTAGAAAAATTTTTTAAAGAGCCAGCT	3240
QY	3241	CAAGCAATATTAATGAAGTAGTGTCCAGTACTAATGAATGGGCTCCAGTATTATGA	3300
Db	3241	CAAGCAATATTAATGAAGTAGTGTCCAGTACTAATGAATGGGCTCCAGTATTATGA	3300
QY	3301	TAGGTCACGTGATGAAGAACATTCAGACAGAACTAGTGAAGAACAGAGGCCAAATATGA	3360
Db	3301	TAGGTCACGTGATGAAGAACATTCAGACAGAACTAGTGAAGAACAGAGGCCAAATATGA	3360
QY	3361	ATGCGATGCTAGATTTGAGGGTTTTGCAACCTGAGGTCTATPAACAAAGTCTCTCTGGAA	3420
Db	3361	ATGCGATGCTAGATTTGAGGGTTTTGCAACCTGAGGTCTATPAACAAAGTCTCTCTGGAA	3420
QY	3421	GTAATGTGAACATCTGAAATATAAAAAAGCAGAAATNTGAAGAAAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATGTGAACATCTGAAATATAAAAAAGCAGAAATNTGAAGAAAGTAGTTCAGACTGTTA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAACACGCTATGGAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAACACGCTATGGAGTAGTC	3540
QY	3541	ATGCATCTCAGAGTTGTGTCGAGACACGTAATACCTGTTTAATGATGTGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGAGTTGTGTCGAGACACGTAATACCTGTTTAATGATGTGTGAATTAAGG	3600
QY	3601	AAGATACTAGTTTGTCTGAAATGACATTTAAGAAAGTTCTGCTGTTTTTACAAAACGG	3660
Db	3601	AAGATACTAGTTTGTCTGAAATGACATTTAAGAAAGTTCTGCTGTTTTTACAAAACGG	3660

QY	3661	TCGAGAAAGGAGACCTTAGCAGAGAGTCCTAGCCCTTCTCACCCATACACTTTGGCTCAG	3720
Db	3661	TCGAGAAAGGAGACCTTAGCAGAGAGTCCTAGCCCTTCTCACCCATACACTTTGGCTCAG	3720
QY	3721	GTTACCGAAGGGGGCCAGAAATTAGAGTCCTCAGACAGAGAACTTATCTAGTGAAGT	3780
Db	3721	GTTACCGAAGGGGGCCAGAAATTAGAGTCCTCAGACAGAGAACTTATCTAGTGAAGT	3780
QY	3781	AAGAGCTCCCTGCTCCAAACACTTGTATTGTTAAAGTAAACAATATACCTCTCAGT	3840
Db	3781	AAGAGCTCCCTGCTCCAAACACTTGTATTGTTAAAGTAAACAATATACCTCTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGCTTGCTACGAGTCGTCTCTAAGAACACAGAGGAATTTT	3900
Db	3841	CTACTAGGCATAGCACCGCTTGCTACGAGTCGTCTCTAAGAACACAGAGGAATTTT	3900
QY	3901	TATCATTTGAATAAGGTTTAAATGACTGCGCTAACCCAGGTAATATTGGCAAGGCATCC	3960
Db	3901	TATCATTTGAATAAGGTTTAAATGACTGCGCTAACCCAGGTAATATTGGCAAGGCATCC	3960
QY	3961	AGGAACATCACCTTAGTAGAGAAACAATAATGTTCTGCTAGCTTGTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAATAATGTTCTGCTAGCTTGTTTCTTCACAGTCA	4020
QY	4021	GTTGAATTGGAAAGCTTAGCTGCAATATCAAAACCCAGATCCTTCTTGATTGGTCTT	4080
Db	4021	GTTGAATTGGAAAGCTTAGCTGCAATATCAAAACCCAGATCCTTCTTGATTGGTCTT	4080
QY	4081	CCAAACAAATAGGCATACGTCGTGAAGCCAGGAGCTTGCTGAGTGACAGAAATGG	4140
Db	4081	CCAAACAAATAGGCATACGTCGTGAAGCCAGGAGCTTGCTGAGTGACAGAAATGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAATAATATCAAGAGACAAACA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAATAATATCAAGAGACAAACA	4200
QY	4201	TGGATTCAACTTAGTGGAAGCACATCTGGGTGTGAGAGTGAAACAGCGTCTCTGAAG	4260
Db	4201	TGGATTCAACTTAGTGGAAGCACATCTGGGTGTGAGAGTGAAACAGCGTCTCTGAAG	4260
QY	4261	ACTGTCAGGGCTATCCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGTCAGGGCTATCCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGATACCATGC	4320
QY	4321	AACATTAACCTATAACCTCCAGCAGAGAAATGGCTAATAGAGCTGTGTAGAACAGC	4380
Db	4321	AACATTAACCTATAACCTCCAGCAGAGAAATGGCTAATAGAGCTGTGTAGAACAGC	4380
QY	4381	ATGGAGCCAGCCTTCTTAACAGCTTACCCTTCATCATTAAGTAGACCTTCTGCCCCTTGAAG	4440
Db	4381	ATGGAGCCAGCCTTCTTAACAGCTTACCCTTCATCATTAAGTAGACCTTCTGCCCCTTGAAG	4440
QY	4441	ACCTGCGAAATCCGAAACAAGCACATCAAAAAACCAATATTAACTTACAGAAAAGTA	4500
Db	4441	ACCTGCGAAATCCGAAACAAGCACATCAAAAAACCAATATTAACTTACAGAAAAGTA	4500
QY	4501	GTTGAATACCTATAAGCCAGATATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTCTCG	4560
Db	4501	GTTGAATACCTATAAGCCAGATATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTCTCG	4560
QY	4561	CAGATAGTTTACCAGTAAAAATTAAGAACACAGAGATGGAAGGTCATCCCTCTTAAT	4620
Db	4561	CAGATAGTTTACCAGTAAAAATTAAGAACACAGAGATGGAAGGTCATCCCTCTTAAT	4620
QY	4621	GCCCATCTTATGATGATAGTGGTACATGCAAGTTGCTCTGGAGTCTTCAGAAATAGA	4680
Db	4621	GCCCATCTTATGATGATAGTGGTACATGCAAGTTGCTCTGGAGTCTTCAGAAATAGA	4680
QY	4681	ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTATGTAAGAGGACAAACGCTGGAAG	4740
Db	4681	ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTATGTAAGAGGACAAACGCTGGAAG	4740
QY	4741	AGTCTGGGCCACAGATTTTACGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGGA	4800

Db 4741 AGTGTGGCCACACGATTGTGAGGAACATCTTACTTGCACAGGAAAGATCTAGAGGGNA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTGGAATGATCCCTCG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTGGAATGATCCCTCG 4860  
Qy 4861 AAGACAGAGCCCCAGAGTCTGTGTTGGACATACCATCTTCACACCTCTGCATTGA 4920  
Db 4861 AAGACAGAGCCCCAGAGTCTGTGTTGGACATACCATCTTCACACCTCTGCATTGA 4920  
Qy 4921 AAGTTCCTGGAATGGAATCTGCAAGATCTGCCCAAGTCCAGCTCTGTCTACTACTG 4980  
Db 4921 AAGTTCCTGGAATGGAATCTGCAAGATCTGCCCAAGTCCAGCTCTGTCTACTACTG 4980  
Qy 4981 ATACTGCTGGGTATATATGATGAGAAAGTGTGAGCAGGAGAGAGCAGAAATGAGAG 5040  
Db 4981 ATACTGCTGGGTATATATGATGAGAAAGTGTGAGCAGGAGAGAGCAGAAATGAGAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCAGTGTGTGCTGAGCCGACAGAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCAGTGTGTGCTGAGCCGACAGAG 5100  
Qy 5101 AATTATGCTGCTGACAAAGTTGGCAAAAACACATCATTACTTAACTAATTA 5160  
Db 5101 AATTATGCTGCTGACAAAGTTGGCAAAAACACATCATTACTTAACTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTATGAAACAGATGCTGAGTTGTGTGAGAGGAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTATGAAACAGATGCTGAGTTGTGTGAGAGGAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTACTTCTGAGTACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTACTTCTGAGTACCC 5280  
Qy 5281 AGCTATTTAAAGAAAGAAATGCTGATGATGAGCATTTTGAAGTTCAGAGAGATG 5340  
Db 5281 AGCTATTTAAAGAAAGAAATGCTGATGATGAGCATTTTGAAGTTCAGAGAGATG 5340  
Qy 5341 TCAATGGAAGAAACCCAGAGTCCAAAGCAGAGCAAGAAATCCAGAGCAGAAAGAT 5400  
Db 5341 TCAATGGAAGAAACCCAGAGTCCAAAGCAGAGCAAGAAATCCAGAGCAGAAAGAT 5400  
Qy 5401 TCAGGGGGCTAGAAATGTTGCTATGAGGCTTCCACCAATGCCCCAGATCAATG 5460  
Db 5401 TCAGGGGGCTAGAAATGTTGCTATGAGGCTTCCACCAATGCCCCAGATCAATG 5460  
Qy 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520  
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520  
Qy 5521 GCAAGAGTGTCCACCAATGTTGTGAGCAGATGCTGAGCAGAGAGAGATGCT 5580  
Db 5521 GCAAGAGTGTCCACCAATGTTGTGAGCAGATGCTGAGCAGAGAGAGATGCT 5580  
Qy 5581 TCCATGCAATTTGGGCAATGTTGAGGACCTGTGAGGACCCGAGAGTGGTGTGAGCA 5640  
Db 5581 TCCATGCAATTTGGGCAATGTTGAGGACCTGTGAGGACCCGAGAGTGGTGTGAGCA 5640  
Qy 5641 GTGTAGCAGCTCTACAGATGTCAGAGAGCTGACACCTACTGATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCAGCTCTACAGATGTCAGAGAGCTGACACCTACTGATACCCAGATCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 8  
LOCUS HSU14680 5711 bp mRNA PRI 05-AUG-1995  
DEFINITION Human breast and ovarian cancer susceptibility (BRCA1) mRNA,  
complete cds.

ACCESSION U14680  
ID 9555931  
KEYWORDS human  
SOURCE Homo sapiens  
ORGANISM human  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Miki Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harshman K., Tavtigian S., Liu Q., Cochran C., Bennett L.M., Ding W., Bell R., Rosenthal J., Hussey C., Tran T., McClure M., Frye C., Hattler T., Phelps R., Haugen-Strano A., Katcher H., Yakumo K., Gholami Z., Shaffer D., Stone S., Beyer S., Wray C., Bogden R., Dayanath P., Ward J., Tonin P., Narod S., Bristow P.K., Norris F.H., Helvering L., Morrison P., Rostek P., Lai M., Barrett J.C., Lewis C., Neuhausen S., Cannon-Albright L., Goldgar D., Wiseman R., Knab A. and Skolnick M.H.  
TITLE A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1  
JOURNAL Science 266 (5182), 66-71 (1994)  
MEDLINE 95025896  
REFERENCE 2 (bases 1 to 5711)  
AUTHORS Skolnick M.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA  
FEATURES  
source  
5'UTR  
exon  
exon  
exon  
gene  
CDS  
location/Qualifiers  
1..5711  
/organism="Homo sapiens"  
/note="For sequence of alternatively spliced exon 4, see GenBank Accession Number U15595"  
/db\_xref="taxon:9606"  
/chromosome="17"  
/map="17q21; spans D17S855"  
1..119  
1..100  
/number=1  
101..199  
/number=2  
120..5711  
/gene="BRCA1"  
120..5711  
/gene="BRCA1"  
/note="Influences susceptibility to breast and ovarian cancer"  
/codon\_start=1  
/db\_xref="PID:9555932"  
/translation="MDLSALRYEYONVYINAKQILIECPICIELEIKPEVSTKCDHIFC  
KFCMLKLINOKRGPSCPLKNDIKRSLOESTRPSQVEELIKITICAFOLDGLEVA  
NSYFNPAKKNENPBEHLKDEVSIIOSMGYRNRAKRLJOSEPNPSLOESTSVOLNSG  
TVRLTRKORIQPORTSVYIELGSSSDYDYNKATYCGVGOELIOTPOSTREIL  
DSAKRACERSETDYTNENHOPRNDLNTTEKRAEHPKRYGSSSVNLHYPCST  
NTHASSLOHENSLLITTDKNAYEAKFCNKSQOGLARSOHNWAGSKETCDNRTP  
STEKVYDLNADPLCEKEMNKQKPLCSNPEDTEVPIWTLNNSIQKNEMFESHDEL  
LGSDSHDESSNAKVAADVLDVLENEVEYSGSSKEDILLASDPHEALIKSEVHAK  
SVESINIEKIFGKTYRKRAKSLPNLSHVENLIGAFVEPOIIORPLTNKLRKRP  
TSGLHPDEIRKADLAVOKTPENINOGNOREONGOVANNITNSHMKTKTQSONK  
NNPLIESLEKSAPEKTAPEPTSSSNMELNLNHNKAPKNNLRKRSRTHIALE  
LYVSRNLPSPNCTEILQDSCSSSEIKKKNOMVRNRNLQLEGEKEPATGAKKN  
KPNQTSKRHSDTEPELKLITNAPGSFPCNTSELKFEVNPISLREKEKELTIVY  
SNMADPDMDLMSGERVYLQTERSVSSISLVPQDYGTORSISLLEVTSLGAKTEP  
NKCYSOCAFENPKGLIHGCSKDNNDTEGFKYPLGHEVNHRSRETSLIEMSESLDAY  
LQNTFRVRSROSAFENPBGNAEEECATFEAHSKISIKKSPKTFPECEKPENGKRE  
SNKPVQVYNTIAGPPYVGQDKPYDAKCSIKGSRCLSQSRGNETGILITNKKG  
LIQNPYRIPPEPIKSEVTKCKKNKLSENEEESHSPEREMGENIPSTVSTISRN  
IRENVFKASSNINEVGSSTNEVSSINEJSSDENPDELIGRNRPKINAMARLQV  
LQPEYVKQSLPQSNCKHPEIKQOEYEVVQVNTDFSLYLSIDLQPMKSSHASQVC  
SETPDLDLDGEEKEDTSFAENDIKESGAVSKSVQGEISRSPSPTHHILAGVGR  
GAKKLESSEENISEDELPCOHLILCKYNNITPSOSTRSTVATBELSKNTENLIS  
LKNSLNDSONVYILAKASQEHHLSEETKCSLFSQCSLELIDITANTNTQDPLIGS  
SKQMRHQSSEGVGLSKDEIVSDDERQGTGLENNQDEOSDNLNGBAAGCSESV  
SEDCGSLSSQSDILITTOORDTMOHNLKIQDEMAELBAVLVEIQHSGSPSNYSPTIISDS

SALDEAPSPIDMUSSEKAVATLISOKASSPILISQBELLSADKREVSADSTANKREKRE  
 RSPSSKAPSPIDMUSMISGSGSLQNNNTISQBELLSADKREVSADSTANKREKRE  
 LIPRODGETPYLESSLSFSDDESPDSRDEPESARKGNTSISATKQVLKVAASS  
 AOSPAARHTDITJGMEETSSAREPDELTAETVENKMSVMSGLPFEELMAYV  
 ARKHITLITLITENAYESSVAVKADREKLEFELJAGKNGVSVFVOTSSIKER  
 KMLNEHEFVRGVAVMRSNNGQKRRABESODRIRGELICOCYGFMTPIIDOLEMMV  
 OLCASSVYKELSTLGTGHTPIVAVDPAMTJEDNGFHALIGMCAPVITRENDLDSV  
 LVIQCEVLELIPOLPHSYT



```
|||||
Db 3181 GTACAGTACGACATTTAGCCGTATTAACATTAGAGAAAAGTTTAAACACCCAGCT 3240
Qy 3241 CAACCAATATTAAATGAAGTAGTTCACAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300
Db 3241 CAACCAATATTAAATGAAGTAGTTCACAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300
Qy 3301 TAGGTTCCAGTATGAGAAAACATTCAAGCAGAACTAGTAGTAAGAACAGAGGCCAAATTTGA 3360
Db 3301 TAGGTTCCAGTATGAGAAAACATTCAAGCAGAACTAGTAGTAAGAACAGAGGCCAAATTTGA 3360
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTGGCACTGAGTCTATTAACAAAGCTTCTCGGAA 3420
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGGCACTGAGTCTATTAACAAAGCTTCTCGGAA 3420
Qy 3421 GTAATTGTAACATCTCGAATAATTAAGAAAGCAAGATATGAAGATAGTTACAGCTGTTA 3480
Db 3421 GTAATTGTAACATCTCGAATAATTAAGAAAGCAAGATATGAAGATAGTTACAGCTGTTA 3480
Qy 3481 ATACAGATTTCTTCATATCTGATTTACATTAAGAAAGCTTATGGAAGCTTATGGAAGTATC 3540
Db 3481 ATACAGATTTCTTCATATCTGATTTACATTAAGAAAGCTTATGGAAGCTTATGGAAGTATC 3540
Qy 3541 ATGATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAG 3600
Db 3541 ATGATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAG 3600
Qy 3601 AAGTACTAGTTTGTCTGAAAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660
Db 3601 AAGTACTAGTTTGTCTGAAAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660
Qy 3661 TCCGAAAAGGAGACCTTAGCGAGAGTCTACCCCTTCACCCATACATTTGGCTCAGG 3720
Db 3661 TCCGAAAAGGAGACCTTAGCGAGAGTCTACCCCTTCACCCATACATTTGGCTCAGG 3720
Qy 3721 GTTCCGAGAGGGGGCCAGAAATTAGAGTCTCAGAAAGAACTTATCTGTAGAGATG 3780
Db 3721 GTTCCGAGAGGGGGCCAGAAATTAGAGTCTCAGAAAGAACTTATCTGTAGAGATG 3780
Qy 3781 AAGAGCTTCCCTGCTCCACACTTGTATTTGGTAAAGTAACAAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTCCACACTTGTATTTGGTAAAGTAACAAATATACCTTCTCAGT 3840
Qy 3841 CTACTAGGCAATGACACGCTGCTACCGAGTCTGTCTTAACACACAGAGAGATTTAT 3900
Db 3841 CTACTAGGCAATGACACGCTGCTACCGAGTCTGTCTTAACACACAGAGAGATTTAT 3900
Qy 3901 TATCATTTGAAGATAGCTTAAATGACTGCACTAACCAGGTAAATTTGSCAAAGGCAATCTC 3960
Db 3901 TATCATTTGAAGATAGCTTAAATGACTGCACTAACCAGGTAAATTTGSCAAAGGCAATCTC 3960
Qy 3961 AGAAGCATACACTTAGTGAGGAAAACAAATGTCTGCTAGCTTTCTTCTCACAGTGCA 4020
Db 3961 AGAAGCATACACTTAGTGAGGAAAACAAATGTCTGCTAGCTTTCTTCTCACAGTGCA 4020
Qy 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACACCCAGAGATCTTTCTGATTTGGTCTT 4080
Db 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACACCCAGAGATCTTTCTGATTTGGTCTT 4080
Qy 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTACAGAAATTTGG 4140
Db 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTACAGAAATTTGG 4140
Qy 4141 TTTGAGATGATGAGAAAGAGGAAAGGGCTTGAAGAAATATCAAGAAAGAGCAAAAGCA 4200
Db 4141 TTTGAGATGATGAGAAAGAGGAAAGGGCTTGAAGAAATATCAAGAAAGAGCAAAAGCA 4200
Qy 4201 TGGATTTCAAATTTAGGTGAAACAGCATTTGGGTGTGAGAGTGAACAAAGCTCTCTGAG 4260
Db 4201 TGGATTTCAAATTTAGGTGAAACAGCATTTGGGTGTGAGAGTGAACAAAGCTCTCTGAG 4260
Qy 4261 ACTGCTAGGGCTATCCCTCAGAGTGCATTTAACACACAGAGGATACCATGC 4320
|||||
Db 4261 ACTGCTAGGGCTATCCCTCAGAGTGCATTTAACACACAGAGGATACCATGC 4320
Qy 4321 AACATAACCTGATTAACCTCCAGCAGGAAAATGGCTGAACTAGAAAGCTGTATTAGACAGC 4380
Db 4321 AACATAACCTGATTAACCTCCAGCAGGAAAATGGCTGAACTAGAAAGCTGTATTAGACAGC 4380
Qy 4381 ATGGGAGCCAGCCTTCTTAACAGCTACCTTTCATATAGTACTCTTTCGCCCTTAGG 4440
Db 4381 ATGGGAGCCAGCCTTCTTAACAGCTACCTTTCATATAGTACTCTTTCGCCCTTAGG 4440
Qy 4441 ACCGGAAGAAATCCAGAACAAAGCAGATCAGAAAAGAGATTAATTAACCTTCAGAAAAAGTA 4500
Db 4441 ACCGGAAGAAATCCAGAACAAAGCAGATCAGAAAAGAGATTAATTAACCTTCAGAAAAAGTA 4500
Qy 4501 GTGAATACCCCTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTCTG 4560
Db 4501 GTGAATACCCCTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAGGTCTG 4560
Qy 4561 CAGATATTTCTACAGTAAATAATTAAGAACACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Db 4561 CAGATATTTCTACAGTAAATAATTAAGAACACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Qy 4621 GCCCATCATTAAGATGATGAGTGTACATGCAAGTTCCTGCGGAGTCTTCAGAAATGAA 4680
Db 4621 GCCCATCATTAAGATGATGAGTGTACATGCAAGTTCCTGCGGAGTCTTCAGAAATGAA 4680
Qy 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGACCAACAGCTGAGAG 4740
Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGACCAACAGCTGAGAG 4740
Qy 4741 AGTCTGGGCCACACAGATTTGACGGAAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCCACACAGATTTGACGGAAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA 4800
Qy 4801 CCCCTTACCTGSAATCTGSAATCAGCTCTCTCTGATGACCCGAAATCGATCCTCTG 4860
Db 4801 CCCCTTACCTGSAATCTGSAATCAGCTCTCTCTGATGACCCGAAATCGATCCTCTG 4860
Qy 4861 AAGACAGAGCCCGCAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920
Db 4861 AAGACAGAGCCCGCAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920
Qy 4921 AAGTCCCAATTGAAGTTGACAGATCTGCCCCAGAGTCCAGCTGCTGCTCATACTG 4980
Db 4921 AAGTCCCAATTGAAGTTGACAGATCTGCCCCAGAGTCCAGCTGCTGCTCATACTG 4980
Qy 4981 ATACTGCTGGTAAATGACATGGAAGAGTGTGACAGAGGAGAACCCGAATTTGACAG 5040
Db 4981 ATACTGCTGGTAAATGACATGGAAGAGTGTGACAGAGGAGAACCCGAATTTGACAG 5040
Qy 5041 CTTCAACAGAAAGGGTCAACAAAAGAAATGTCATGTGTGTGCTGCGCTGACCCAGAG 5100
Db 5041 CTTCAACAGAAAGGGTCAACAAAAGAAATGTCATGTGTGTGCTGCGCTGACCCAGAG 5100
Qy 5101 AATTTATGCTGCTGTACAAAGTTGCCCCAGAAAACACACATCACTTTAACTAATTA 5160
Db 5101 AATTTATGCTGCTGTACAAAGTTGCCCCAGAAAACACACATCACTTTAACTAATTA 5160
Qy 5161 CTGAAGAGACTACATGATTTGTTATGAAAACAGATGCTGAGTTGTGTGAACGGCAC 5220
Db 5161 CTGAAGAGACTACATGATTTGTTATGAAAACAGATGCTGAGTTGTGTGAACGGCAC 5220
Qy 5221 TGAATATTTTCTAGAAATTCGGGAGGAAAATGGTAGTTAGCTATTCTGGGTGACC 5280
Db 5221 TGAATATTTTCTAGAAATTCGGGAGGAAAATGGTAGTTAGCTATTCTGGGTGACC 5280
Qy 5281 AGTCTATTTAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340
Db 5281 AGTCTATTTAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340
Qy 5341 TCAATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGAGAAATCCACAGAGAGAAAGATCT 5400
Db 5341 TCAATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGAGAGAAATCCACAGAGAGAAAGATCT 5400
```



QY 5401 TCAGGGGCTAGAAATGTGTGTAATGGCCCTTACCAACATGCCACAGATCAACTGG 5460  
| | | | |  
DB 5401 TCAGGGGCTAGAAATGTGTGTAATGGCCCTTACCAACATGCCACAGATCAACTGG 5460  
| | | | |  
QY 5461 AATGAGATGACAGCTGTGTGCTTCTGTGTGAAGAGACTTTCATCATTCACCCCTG 5520  
| | | | |  
DB 5461 AATGAGATGACAGCTGTGTGCTTCTGTGTGAAGAGACTTTCATCATTCACCCCTG 5520  
| | | | |  
QY 5521 GCACAGGTGTCCACCAATGTGTGTGACAGCAGATGCTTGACAGAGACATGAGCT 5580  
| | | | |  
DB 5521 GCACAGGTGTCCACCAATGTGTGTGACAGCAGATGCTTGACAGAGACATGAGCT 5580  
| | | | |  
QY 5581 TCCATGCAATTTGGGACAGATGTGTGAGCAGCTGTGTGTGACCCGAGAGTGGGTGTGACA 5640  
| | | | |  
DB 5581 TCCATGCAATTTGGGACAGATGTGTGAGCAGCTGTGTGTGACCCGAGAGTGGGTGTGACA 5640  
| | | | |  
QY 5641 GTGTAGCACTCTACCAATGTCAGAGAGCTGACACTACCTGATACCCAGATCCCCACA 5700  
| | | | |  
DB 5641 GTGTAGCACTCTACCAATGTCAGAGAGCTGACACTACCTGATACCCAGATCCCCACA 5700  
| | | | |  
QY 5701 GCCACTACTGA 5711  
| | | | |  
DB 5701 GCCACTACTGA 5711  
| | | | |  
RESULT 9  
LOCUS 140795 5711 bp DNA PAT 01-MAY-1997  
DEFINITION Sequence 4 from patent US 5622829.  
ACCESSION 140795  
NID 92082275  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS King, M., Friedman, L., Ostremeyer, B., Rowell, S., Lynch, E., Szabo, C.  
and Lee, M.  
TITLE Genetic markers for breast, ovarian, and prostatic cancer  
JOURNAL Patent: US 5622829-A 4 22-APR-1997;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1956 a 1099 c 1275 g 1381 t  
ORIGIN

Query Match 99.9%; Score 5707.8; DB 6; Length 5711:  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCTGCTGAGACTCTCTGACCCCGACAGGCTGTGGGTTTCAGATTAATGAGGC 60  
| | | | |  
DB 1 ACCTGCTGAGACTCTCTGACCCCGACAGGCTGTGGGTTTCAGATTAATGAGGC 60  
| | | | |  
QY 61 CCTGGCTAGAGAGGCTTACCCCTCTGCTCTGGTGAATTCATTGGAACAGAAAGAA 120  
| | | | |  
DB 61 CCTGGCTAGAGAGGCTTACCCCTCTGCTCTGGTGAATTCATTGGAACAGAAAGAA 120  
| | | | |  
QY 121 TGGATTATCTGCTCTTGGGTTGAAGAAGTACAAATGCTAATATGATGCAAGAAA 180  
| | | | |  
DB 121 TGGATTATCTGCTCTTGGGTTGAAGAAGTACAAATGCTAATATGATGCAAGAAA 180  
| | | | |  
QY 181 TCTTAGAGTGTCCCATCTGTGTGAGATGTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
| | | | |  
DB 181 TCTTAGAGTGTCCCATCTGTGTGAGATGTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
| | | | |  
QY 241 ACATATTTTGCAGATTTTGCATGCTGTAAGAACTTCTCAACGAGAAAGAGGCTTCAAGT 300  
| | | | |  
DB 241 ACATATTTTGCAGATTTTGCATGCTGTAAGAACTTCTCAACGAGAAAGAGGCTTCAAGT 300  
| | | | |  
QY 301 GTCTTTATGTAAAGATGATATACCAAAAGAGGCTTACAGAAAGTACAGATTTAGTC 360  
| | | | |

DB 301 GTCTTTATGTAAAGATGATATACCAAAAGAGGCTTACAGAAAGTACAGATTTAGTC 360  
| | | | |  
QY 361 AACTTGTGAAGAGCTATTGAATCATTTGCTTTTACAGTTGACAGAGTTGGAGT 420  
| | | | |  
DB 361 AACTTGTGAAGAGCTATTGAATCATTTGCTTTTACAGTTGACAGAGTTGGAGT 420  
| | | | |  
QY 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
| | | | |  
DB 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
| | | | |  
QY 481 AAGTTTATATCAACAAAGTATGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540  
| | | | |  
DB 481 AAGTTTATATCAACAAAGTATGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540  
| | | | |  
QY 541 AACCCGAAATTCCTCTCTTCCAGAAACCAAGTCTGATGCTCAACTCTTAACCTTGGAA 600  
| | | | |  
DB 541 AACCCGAAATTCCTCTCTTCCAGAAACCAAGTCTGATGCTCAACTCTTAACCTTGGAA 600  
| | | | |  
QY 601 CTGTGAGAACTGTAGAGACAAAGCAGCGATACACCTCAAAAGAGCTGTCTACATTTG 660  
| | | | |  
DB 601 CTGTGAGAACTGTAGAGACAAAGCAGCGATACACCTCAAAAGAGCTGTCTACATTTG 660  
| | | | |  
QY 661 AATTGGATCTGATTTCTTCTGAAAGATACCGTTATATAGCAACTTATTCAGATGGAG 720  
| | | | |  
DB 661 AATTGGATCTGATTTCTTCTGAAAGATACCGTTATATAGCAACTTATTCAGATGGAG 720  
| | | | |  
QY 721 ATCAAGATTTGTTACAAATCACCCCTCAAGAACCGGATGAATACGTTGGATTCG 780  
| | | | |  
DB 721 ATCAAGATTTGTTACAAATCACCCCTCAAGAACCGGATGAATACGTTGGATTCG 780  
| | | | |  
QY 781 CAAAAAAGGCTGCTTGTGATTTTCTGAGACGGATGTAACTAATCTGACATCATCAAC 840  
| | | | |  
DB 781 CAAAAAAGGCTGCTTGTGATTTTCTGAGACGGATGTAACTAATCTGACATCATCAAC 840  
| | | | |  
QY 841 CCAGTATATATGATTTTGAACACACACACAGACGCTGACAGTACAGCAAAAAGT 900  
| | | | |  
DB 841 CCAGTATATATGATTTTGAACACACACACAGACGCTGACAGTACAGCAAAAAGT 900  
| | | | |  
QY 901 ATCAGGATGTTCTGTTTAACTGATGATGAGGACATGAGGCAAAATCTCTGCA 960  
| | | | |  
DB 901 ATCAGGATGTTCTGTTTAACTGATGATGAGGACATGAGGCAAAATCTCTGCA 960  
| | | | |  
QY 961 GCTCATTAACAGATGAGAACACAGCTTTATTACTCACTAAGACAGAAATGATGTAGAAA 1020  
| | | | |  
DB 961 GCTCATTAACAGATGAGAACACAGCTTTATTACTCACTAAGACAGAAATGATGTAGAAA 1020  
| | | | |  
QY 1021 AGGCTGAATTTCTGTTAATAAAGCAAAAGCCTGGCTTACAGAGGAGCCACATACAGAT 1080  
| | | | |  
DB 1021 AGGCTGAATTTCTGTTAATAAAGCAAAAGCCTGGCTTACAGAGGAGCCACATACAGAT 1080  
| | | | |  
QY 1081 GGGCTGGAAGTAAAGAAACATGATATGATGAGGAGCACTCCAGCACAAGAAAAAGTAG 1140  
| | | | |  
DB 1081 GGGCTGGAAGTAAAGAAACATGATATGATGAGGAGCACTCCAGCACAAGAAAAAGTAG 1140  
| | | | |  
QY 1141 ATCTGAATGCTATCCCTGTGTGTGAGAGAAAGATGAATTAAGCAGAAATGCCATGCT 1200  
| | | | |  
DB 1141 ATCTGAATGCTATCCCTGTGTGTGAGAGAAAGATGAATTAAGCAGAAATGCCATGCT 1200  
| | | | |  
QY 1201 CAGAGAACTCTAGAGATGATGAGAGATGTTCTGTGATTAACACTAATATGCGCATTCGA 1260  
| | | | |  
DB 1201 CAGAGAACTCTAGAGATGATGAGAGATGTTCTGTGATTAACACTAATATGCGCATTCGA 1260  
| | | | |  
QY 1261 AAGTTATAGTGTGTTTCCAGAGATGATGAGATGTTGTTGATGATGATGATGATGATG 1320  
| | | | |  
DB 1261 AAGTTATAGTGTGTTTCCAGAGATGATGAGATGTTGTTGATGATGATGATGATGATG 1320  
| | | | |  
QY 1321 GGGAGTCTGAATCAAAATGCAAGTATGATGATGATGATGATGATGATGATGATGATG 1380  
| | | | |  
DB 1321 GGGAGTCTGAATCAAAATGCAAGTATGATGATGATGATGATGATGATGATGATGATG 1380  
| | | | |  
QY 1381 AATTTCTGCTTCTCAGAGAAATAGACTTACTGGCCAGTATGCTTCATGAGGCTTTAA 1440  
| | | | |

Db 1381 AATATTCGTGCTTCTCAGAGAAATAGACTTGTGCGCCAGTATCTCTAGCGCTTTAA 1440  
Oy 1441 TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATATATTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATATATTGAAGCAAAATAT 1500  
Oy 1501 TTGGGAAAACCTATGGGAAGGAAGGCAAGCCTCCCACTTAAAGCCATGTAACTGAAATC 1560  
Db 1501 TTGGGAAAACCTATGGGAAGGAAGGCAAGCCTCCCACTTAAAGCCATGTAACTGAAATC 1560  
Oy 1561 TAATATAGAGCATTTTGTACTGAGCCACAGATATATACAGAGGCTCCCTCACAAATA 1620  
Db 1561 TAATATAGAGCATTTTGTACTGAGCCACAGATATATACAGAGGCTCCCTCACAAATA 1620  
Oy 1621 AATTAAGCGTAAAAGAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAAGAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Oy 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATATATAGGGAATTAACCAAGCGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATATATAGGGAATTAACCAAGCGAGC 1740  
Oy 1741 AGAATGTCAAGTGAATGATATTTACTAATAGTGTGTCATGAGATTAACCAAGGATTT 1800  
Db 1741 AGAATGTCAAGTGAATGATATTTACTAATAGTGTGTCATGAGATTAACCAAGGATTT 1800  
Oy 1801 CTATTCAGATGAGAAAAATCTTAACCCAAATAGAAATCACTCGAAAAAGATCTGTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCCAAATAGAAATCACTCGAAAAAGATCTGTTTCA 1860  
Oy 1861 AAACGAAAGCTAACCCTATTAACAGCAGATATTAAGCAATATGGAATCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTAACCCTATTAACAGCAGATATTAAGCAATATGGAATCGAATTAATATCC 1920  
Oy 1921 ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGGAGAACTCTTCCAGAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGGAGAACTCTTCCAGAGCATATTC 1980  
Oy 1981 ATGCGCTTGAACTAGTACTAGTAAATCTAAGCCACCACTAATTTGTAAGTTCAAA 2040  
Db 1981 ATGCGCTTGAACTAGTACTAGTAAATCTAAGCCACCACTAATTTGTAAGTTCAAA 2040  
Oy 2041 TTGATATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAAGTACACCAATGCCAGTCA 2100  
Db 2041 TTGATATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAAGTACACCAATGCCAGTCA 2100  
Oy 2101 GGCACAGCAGAAACCTACACTCATGAGAGTAAAGAACTGCAACTGGAGCCAGAAAGA 2160  
Db 2101 GGCACAGCAGAAACCTACACTCATGAGAGTAAAGAACTGCAACTGGAGCCAGAAAGA 2160  
Oy 2161 GTAAACAGCCAAATGAGACAGACATGAAAAAGCATGACAGCATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAGACAGACATGAAAAAGCATGACAGCATCTTCCAGAGCTGA 2220  
Oy 2221 AGTTAAACAAATCAGCTGCTTCTTTACTTAAGTGTTCAAATACAGTGAACCTTAAAGAT 2280  
Db 2221 AGTTAAACAAATCAGCTGCTTCTTTACTTAAGTGTTCAAATACAGTGAACCTTAAAGAT 2280  
Oy 2281 TTGTCAATCTCTAGCTTCCCAAGAGAAAGAAAGAGAACTAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTCTAGCTTCCCAAGAGAAAGAAAGAGAACTAGAAACAGTTAAAGTGT 2340  
Oy 2341 CTAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAAACTG 2400  
Db 2341 CTAATTAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAAACTG 2400  
Oy 2401 AAAGATCTCTAGAGTAGAGTACATTTTATTTGTAAGTGTGTACTGATTTAGGCACTCAGG 2460  
Db 2401 AAAGATCTCTAGAGTAGAGTACATTTTATTTGTAAGTGTGTACTGATTTAGGCACTCAGG 2460  
Oy 2461 AAAGATCTCTCTAGAGTAGAGTACATCTAGAGAGGCAAAACAGAACTAAAT 2520  
Db 2461 AAAGATCTCTCTAGAGTAGAGTACATCTAGAGAGGCAAAACAGAACTAAAT 2520

Oy 2521 GTGTAGTCAAGTGTGACACATTTGAAAAACCCCAAGGACATTAATTCAGTGTGTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACACATTTGAAAAACCCCAAGGACATTAATTCAGTGTGTTCCAAAG 2580  
Oy 2581 ATAAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATTAAGTTAACCAAGT 2640  
Db 2581 ATAAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATTAAGTTAACCAAGT 2640  
Oy 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGCAATATACAT 2700  
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGCAATATACAT 2700  
Oy 2701 TCAAGTTTCAAAAGCGCAGTCTATTGCTCTGTTTCAATTCAGAAATGCAAGAGG 2760  
Db 2701 TCAAGTTTCAAAAGCGCAGTCTATTGCTCTGTTTCAATTCAGAAATGCAAGAGG 2760  
Oy 2761 AATGTGCAACATCTCTCTCCCACTCTGGGCTCTTAAAGAAACAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTCTCCCACTCTGGGCTCTTAAAGAAACAGTCCAAAGTCACTT 2820  
Oy 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Oy 2881 AGACAGTTAATATCACTCAGGCTTCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTCAGGCTTCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Oy 2941 ATGCCAAATGTATGTCAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGTATGTCAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Oy 3001 AGCAATCTGAGCTCATCTCTCCAAATTAACATGAGCTTTTCAAAAGCCATATGCTATAC 3060  
Db 3001 AGCAATCTGAGCTCATCTCTCCAAATTAACATGAGCTTTTCAAAAGCCATATGCTATAC 3060  
Oy 3061 CACCACTTTTCCCATCAGTCAATTTGTTAAATCTAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAGTCAATTTGTTAAATCTAATGTAAGAAAAATCTGCTAGAGG 3120  
Oy 3121 AAACTTTGAGGACATTCATATGCTAGTGAAGAAATGGGAATTAAGAACTTCCAA 3180  
Db 3121 AAACTTTGAGGACATTCATATGCTAGTGAAGAAATGGGAATTAAGAACTTCCAA 3180  
Oy 3181 GTACAGTGAACAATTTAGCCGTAATTAACATTAAGAAATGTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAACAATTTAGCCGTAATTAACATTAAGAAATGTTTAAAGAGCCAGCT 3240  
Oy 3241 CAAGCAATATTAAATGAAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAAATGAAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Oy 3301 TAGGTTCCAGTATGAAAAACATTCAGCAGAACTAGTGAAGAAAGAGGCCCCAAATGGA 3360  
Db 3301 TAGGTTCCAGTATGAAAAACATTCAGCAGAACTAGTGAAGAAAGAGGCCCCAAATGGA 3360  
Oy 3361 ATGCTATCTTAGATTAGGGGTTTTCGAACCTGAGGCTTATTAACCAAGTCTTCCCTGAA 3420  
Db 3361 ATGCTATCTTAGATTAGGGGTTTTCGAACCTGAGGCTTATTAACCAAGTCTTCCCTGAA 3420  
Oy 3421 GTAATTTGAAGCATCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480  
Db 3421 GTAATTTGAAGCATCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480  
Oy 3481 ATACAGATTTTCTCTCATATCTGATTTAGATTAAGTGAACAGCTTATGGAAGTACTC 3540  
Db 3481 ATACAGATTTTCTCTCATATCTGATTTAGATTAAGTGAACAGCTTATGGAAGTACTC 3540  
Oy 3541 ATGATCTCAGAGTTTGTCTCAGACACCTGATGACCTTGTGATGATGATGTAATTAAGG 3600  
Db 3541 ATGATCTCAGAGTTTGTCTCAGACACCTGATGACCTTGTGATGATGATGTAATTAAGG 3600

QY 3601 AAGATCTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTACGAAAGG 3660  
| | | | |  
Db 3601 AAGATCTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTACGAAAGG 3660  
QY 3661 TCCGAAAGAGAGCTTACGAGAGTCTAGCCCTTACCCATACATATTTGGCTCAG 3720  
| | | | |  
Db 3661 TCCGAAAGAGAGCTTACGAGAGTCTAGCCCTTACCCATACATATTTGGCTCAG 3720  
QY 3721 GTTACCGAAGAGGGGCGCAAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTAGAGATG 3780  
| | | | |  
Db 3721 GTTACCGAAGAGGGGCGCAAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTAGAGATG 3780  
QY 3781 AAGACTTCCCTGCTTCCCAACACTTGTATTTGGTAAAGTAAACATATTAACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGACTTCCCTGCTTCCCAACACTTGTATTTGGTAAAGTAAACATATTAACCTTCTCAGT 3840  
QY 3841 CTACAGAGCTAGCAACCGTGTACCGAGTGTCTTAAGAAACAGAGAGAAATTTAT 3900  
| | | | |  
Db 3841 CTACAGAGCTAGCAACCGTGTACCGAGTGTCTTAAGAAACAGAGAGAAATTTAT 3900  
QY 3901 TATCATTTGAGAAATAGCTTAAATGACTGCAATACCAAGTAAATTTGGCAAGGCACTC 3960  
| | | | |  
Db 3901 TATCATTTGAGAAATAGCTTAAATGACTGCAATACCAAGTAAATTTGGCAAGGCACTC 3960  
QY 3961 AGGACATCACCTTAGTGAGAAACAAATGTCTGCTAGCTTGTCTTCTCAGATGCA 4020  
| | | | |  
Db 3961 AGGACATCACCTTAGTGAGAAACAAATGTCTGCTAGCTTGTCTTCTCAGATGCA 4020  
QY 4021 GTGAATTTGGAAAGCTTGAATGCAATACAAACACCAGATCCTTCTTATTTGTTCTT 4080  
| | | | |  
Db 4021 GTGAATTTGGAAAGCTTGAATGCAATACAAACACCAGATCCTTCTTATTTGTTCTT 4080  
QY 4081 CCAACAAATGAGCATCATGCTGAAGCCAGGAGTGGTCTGAGTGAACAGAAATGG 4140  
| | | | |  
Db 4081 CCAACAAATGAGCATCATGCTGAAGCCAGGAGTGGTCTGAGTGAACAGAAATGG 4140  
QY 4141 TTTCGATGATGAGAAAGAGAGAGGGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200  
| | | | |  
Db 4141 TTTCGATGATGAGAAAGAGAGAGGGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTTCAAATTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAACGCTCTGAAG 4260  
| | | | |  
Db 4201 TGGATTTCAAATTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAACGCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTAACTCAGCAGAGAGGATACCATGC 4320  
| | | | |  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTAACTCAGCAGAGAGGATACCATGC 4320  
QY 4321 AACATTAACCTGATTAAGCTCCAGCAAGAAATGGCTGAATAGAGTGTGTAAGAACAG 4380  
| | | | |  
Db 4321 AACATTAACCTGATTAAGCTCCAGCAAGAAATGGCTGAATAGAGTGTGTAAGAACAG 4380  
QY 4381 ATGGAGCAGGCTTCTAAGCAGCTACCTTCCATCATTAAGTACTTCTGCTTGAAG 4440  
| | | | |  
Db 4381 ATGGAGCAGGCTTCTAAGCAGCTACCTTCCATCATTAAGTACTTCTGCTTGAAG 4440  
QY 4441 ACCTCGCAAAATCCAAACAGACATCGAAAAAGCAGTATTAATCTTACGAAAAAGTA 4500  
| | | | |  
Db 4441 ACCTCGCAAAATCCAAACAGACATCGAAAAAGCAGTATTAATCTTACGAAAAAGTA 4500  
QY 4501 GTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTCTGCTGCAAGTGTGAGGTCTG 4560  
| | | | |  
Db 4501 GTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTCTGCTGCAAGTGTGAGGTCTG 4560  
QY 4561 CAGATAGTCTTACAGTAAATAAAGAAACAGAGTGAAGAGTCAATCCCTTCAAT 4620  
| | | | |  
Db 4561 CAGATAGTCTTACAGTAAATAAAGAAACAGAGTGAAGAGTCAATCCCTTCAAT 4620  
QY 4621 GCCCATCTTATGATATAGTGTGATGACATGCAAGTGTGCTGAGAGTCTTCAAGATAGAA 4680  
| | | | |  
Db 4621 GCCCATCTTATGATATAGTGTGATGACATGCAAGTGTGCTGAGAGTCTTCAAGATAGAA 4680  
QY 4681 ACTACCATCTTCAAGAGAGTCAATTAAGTGTGATGATGAGAGCAACAGCTGGAG 4740  
| | | | |

Db 4681 ACTACCATCTTCAAGAGAGTCAATTAAGTGTGATGATGAGAGCAACAGCTGGAG 4740  
| | | | |  
QY 4741 AGTCTGGGCGCACAGATTTGAGCGAAACATCTTACTTCCAAAGCAGATCTAGAGGAA 4800  
| | | | |  
Db 4741 AGTCTGGGCGCACAGATTTGAGCGAAACATCTTACTTCCAAAGCAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCTGGAATCTGATCTTCTG 4860  
| | | | |  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCTGGAATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCCAGAGTCAAGTGTGTTGGCAACATATCCATCTTCAACCTGATTTGA 4920  
| | | | |  
Db 4861 AAGACAGAGCCCCAGAGTCAAGTGTGTTGGCAACATATCCATCTTCAACCTGATTTGA 4920  
QY 4921 AAGTTCGCCAATTTGAAGTTGAGAAATCTGCCAGAGTCCAGCTGCTGCTATCTACTG 4980  
| | | | |  
Db 4921 AAGTTCGCCAATTTGAAGTTGAGAAATCTGCCAGAGTCCAGCTGCTGCTATCTACTG 4980  
QY 4981 ATACTGCTGGGTATTAATGCAATGCAAGAAATGTGAGCAGGAGAAAGCCAGAAATTTGACAG 5040  
| | | | |  
Db 4981 ATACTGCTGGGTATTAATGCAATGCAAGAAATGTGAGCAGGAGAAAGCCAGAAATTTGACAG 5040  
QY 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGNTGNTGCTGCGCTGACCCAGAG 5100  
| | | | |  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGNTGNTGCTGCGCTGACCCAGAG 5100  
QY 5101 AATTATGCTGCTGTACAAAGTTTGGCAAAAAACACACATCATCTTAATTAATTA 5160  
| | | | |  
Db 5101 AATTATGCTGCTGTACAAAGTTTGGCAAAAAACACACATCATCTTAATTAATTA 5160  
QY 5161 CTGAAGAGCTACTATGTTGTTATGAAGAAACAGATGCTGAGTGTGTTGTGAACGGACAC 5220  
| | | | |  
Db 5161 CTGAAGAGCTACTATGTTGTTATGAAGAAACAGATGCTGAGTGTGTTGTGAACGGACAC 5220  
QY 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATTTTCTGGGTGACCC 5280  
| | | | |  
Db 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATTTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
| | | | |  
Db 5281 AGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCCAGAGGCTCCAAAGCGAGCAAGAAATCCAGAGAGAAAGATCT 5400  
| | | | |  
Db 5341 TCAATGGAAGAAACCCAGAGGCTCCAAAGCGAGCAAGAAATCCAGAGAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCTTACCAACATGCCCCAGAGATCACTGG 5460  
| | | | |  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCTTACCAACATGCCCCAGAGATCACTGG 5460  
QY 5461 AATGATGATACAGCTGTGTGTGCTTGTGTGTAAGAGACCTTTCATTCATCACTCTG 5520  
| | | | |  
Db 5461 AATGATGATACAGCTGTGTGTGCTTGTGTGTAAGAGACCTTTCATTCATCACTCTG 5520  
QY 5521 GCACAGGTGTCCACCCTTGTGTGTGTCAGCCAGATGCTTGAAGAGAGCAAAATGCT 5580  
| | | | |  
Db 5521 GCACAGGTGTCCACCCTTGTGTGTGTCAGCCAGATGCTTGAAGAGAGCAAAATGCT 5580  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACACTGTGTGACCCGAGATGGGTGTGAGCA 5640  
| | | | |  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACACTGTGTGACCCGAGATGGGTGTGAGCA 5640  
QY 5641 GTTAGCAGCTTACAGAGTCCAGAGAGTGAACACCTTACCTGATACCCAGATCCCCACA 5700  
| | | | |  
Db 5641 GTTAGCAGCTTACAGAGTCCAGAGAGTGAACACCTTACCTGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
| | | | |  
Db 5701 GCCACTACTGA 5711  
| | | | |

RESULT 10

Query Match	99.9%;	Score 5707.8;	DB 6;	Length 5711;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5709;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

OY	721	ATCAAGAAATTGTTACAAATATCCACCCCTCCAAAGGAACCAAGSAGTAAATCAAGTTTGATTTCTG	780
Db	721	ATCAAGAAATTGTTACAAATATCCACCCCTCAAGGAACCAAGSAGTAAATCAAGTTTGATTTCTG	780
OY	781	CAAAAAAGGCGCTGTGGATTTTCTGAGCGGAGTGTAACTAATCTGACATCATCTAAC	840
Db	781	CAAAAAAGGCGCTGTGGATTTTCTGAGCGGAGTGTAACTAATCTGACATCATCTAAC	840
OY	841	CCAGTAATTAATGATTTGTAACACCCACTGAGAAAGCGTGCACACTGAGAGGATCCAGAAAGT	900
Db	841	CCAGTAATTAATGATTTGTAACACCCACTGAGAAAGCGTGCACACTGAGAGGATCCAGAAAGT	900
OY	901	ATCAAGGAGTGTCTGTTTCAACTGCTGATGTGAGCCATGTGGCAATAATCTATGCCA	960
Db	901	ATCAAGGAGTGTCTGTTTCAACTGCTGATGTGAGCCATGTGGCAATAATCTATGCCA	960
OY	961	GCTCATTTACAGCANTGANAAGAGAGTTTNTTACTCACTAAACAGAAATGAAATGTAGAA	1020
Db	961	GCTCATTTACAGCANTGANAAGAGAGTTTNTTACTCACTAAACAGAAATGAAATGTAGAA	1020
OY	1021	AGCGTGAATTTCTGTAATTAAGCAAAACACGCTGCTTACAGAGAGCCAACTAACAT	1080
Db	1021	AGCGTGAATTTCTGTAATTAAGCAAAACACGCTGCTTACAGAGAGCCAACTAACAT	1080
OY	1081	GGCGTGAAGTAAGAAACATGTATGATAGGCGGACTCCAGCAGAGAAAAAAGGTAG	1140
Db	1081	GGCGTGAAGTAAGAAACATGTATGATAGGCGGACTCCAGCAGAGAAAAAAGGTAG	1140
OY	1141	ATCTGAATGCTGATCCCTCTGTGTGANAAGAAAGATAGAAATAGCAGAAACTGCCATCT	1200
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGANAAGAAAGATAGAAATAGCAGAAACTGCCATCT	1200
OY	1201	CAGAGAAATCCAGAGATCTCGAAGATGCTTCCTGTGATACTTAATATAGCAGATTCAGA	1260
Db	1201	CAGAGAAATCCAGAGATCTCGAAGATGCTTCCTGTGATACTTAATATAGCAGATTCAGA	1260
OY	1261	AAGTTAATGAGTGGTTTCCAGAAAGTATGAACGTGTAGGTTCTGATGACTCACATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTCCAGAAAGTATGAACGTGTAGGTTCTGATGACTCACATGATG	1320
OY	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATGAGACITTTAAATAGGTAGTG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATGAGACITTTAAATAGGTAGTG	1380
OY	1381	AATATTCCTGGTCTCGAGACAAATATGACTTCTGGCCGAGTATCCTATGAGGCTTTAA	1440
Db	1381	AATATTCCTGGTCTCGAGACAAATATGACTTCTGGCCGAGTATCCTATGAGGCTTTAA	1440
OY	1441	TATGTAAAGTGAAGAGATCTCACTCCAAATCTAGTAGAGTATATTGAGCAAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGATCTCACTCCAAATCTAGTAGAGTATATTGAGCAAAATAT	1500
OY	1501	TTGGAAAAACCTATCGGAGAGAGGCAAGCCTCCCACTTAAGCATGTAACTGAAAATC	1560
Db	1501	TTGGAAAAACCTATCGGAGAGAGGCAAGCCTCCCACTTAAGCATGTAACTGAAAATC	1560
OY	1561	TAAATTAAGAGACATTTGTTACTGAGCCACAGATATACAAAGGTCCTCCCAAAATA	1620
Db	1561	TAAATTAAGAGACATTTGTTACTGAGCCACAGATATACAAAGGTCCTCCCAAAATA	1620
OY	1621	AATTAAGCGTAAAGAGAGACCTCACTACAGGCTTCATCTGAGGATTTTATCAAGAAG	1680
Db	1621	AATTAAGCGTAAAGAGAGACCTCACTACAGGCTTCATCTGAGGATTTTATCAAGAAG	1680
OY	1681	CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAATCAGGAACTAACCAAGCGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAATCAGGAACTAACCAAGCGAGC	1740
OY	1741	AGAAATGTCGAAGTGAAGAAATTAATTAAGTGGTCTAGAGATTAACCAAAAGGTGATT	1800
Db	1741	AGAAATGTCGAAGTGAAGAAATTAATTAAGTGGTCTAGAGATTAACCAAAAGGTGATT	1800
OY	1801	CTAATCAAGATGAGAAAAATCCTTAACCCCAATAGAAATCACTCCAAAAAATAATCTGTTTCA	1860

Db	1801	CTATTGGAATGABAAAAATCTCTAACCATATGAAATCTCGAAAAAGAAATCTGCTTTC	1860
Qy	1861	AAACGAAGCTGAACCTATTAAGCAGCAGTATAGCAATATGAACTGAAATTAATATCC	1920
Db	1861	AAACGAAGCTGAACCTATTAAGCAGCAGTATAGCAATATGAACTGAAATTAATATCC	1920
Qy	1921	ACATTCGAAAAAGCACTTAAAAAGAAATAGGCTGAGAGAGAAATCTTCTACCGGCATATTC	1980
Db	1921	ACATTCGAAAAAGCACTTAAAAAGAAATAGGCTGAGAGAGAAATCTTCTACCGGCATATTC	1980
Qy	1981	ATGGGCTTGAACCTAGTAGTCAGTAGAATCTAACGCCACCTAATTTGTAAGTAATGGCAA	2040
Db	1981	ATGGGCTTGAACCTAGTAGTCAGTAGAATCTAACGCCACCTAATTTGTAAGTAATGGCAA	2040
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAAGTACAGCCAAATGCGCAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAAGTACAGCCAAATGCGCAGTCA	2100
Qy	2101	GGCAGCAGCAGAAACCTTCAACTCTATGGAAGTTAAAGAACTCGCACTGAGGCCAAGAGA	2160
Db	2101	GGCAGCAGCAGAAACCTTCAACTCTATGGAAGTTAAAGAACTCGCACTGAGGCCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAACAGACAGTAAGAAAGACATGACAGAGACTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAACAGACAGTAAGAAAGACATGACAGAGACTTCCAGAGCTGA	2220
Qy	2221	AGTTAACCAAAATGCACCTGCTCTTTCTTAAGTGTCCAAATACCAAGTAACTTAAAGAT	2280
Db	2221	AGTTAACCAAAATGCACCTGCTCTTTCTTAAGTGTCCAAATACCAAGTAACTTAAAGAT	2280
Qy	2281	TTGTCAATCCTACCTTCCAAAGAGAGAAAAAGACAGAACTAGAAACAGTTAAAGTG	2340
Db	2281	TTGTCAATCCTACCTTCCAAAGAGAGAAAAAGACAGAACTAGAAACAGTTAAAGTG	2340
Qy	2341	CTAATATGCTGTAAGAGCCCAAGAGATCTCATGTTAATGAGAAAGGGTTTGCAAACTG	2400
Db	2341	CTAATATGCTGTAAGAGCCCAAGAGATCTCATGTTAATGAGAAAGGGTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCAATGGTACCTGTAAGTATGAGCACTAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCAATGGTACCTGTAAGTATGAGCACTAGG	2460
Qy	2461	AAAGTATCTGCTACTGAGAGATTAGCACTTAGGGAAGGCAAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTGCTACTGAGAGATTAGCACTTAGGGAAGGCAAAAACAGAACCAATTAAT	2520
Qy	2521	GTCGTAGTAGTGTGCAAGCTTTGAAAAACCCCAAGGACATAATTCATGTTTCCAAAG	2580
Db	2521	GTCGTAGTAGTGTGCAAGCTTTGAAAAACCCCAAGGACATAATTCATGTTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCATTTGGGACATGAAGTTAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCATTTGGGACATGAAGTTAACACAGTC	2640
Qy	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTGTAGCTCAGTATTTGACAAATACAT	2700
Db	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTGTAGCTCAGTATTTGACAAATACAT	2700
Qy	2701	TCAAGGTTTCAAGGCCCGAGTCAATTTGCTCTGTTTTCAAATCCAGGAATGCGAAGAGG	2760
Db	2701	TCAAGGTTTCAAGGCCCGAGTCAATTTGCTCTGTTTTCAAATCCAGGAATGCGAAGAGG	2760
Qy	2761	AATGTGCAACATTTCTGCGCACTGTGGGCTTTAAAGAAACAAGGCCCAAAAGTGACTTT	2820
Db	2761	AATGTGCAACATTTCTGCGCACTGTGGGCTTTAAAGAAACAAGGCCCAAAAGTGACTTT	2820
Qy	2821	TTGAATGTGACAAAAAGGAAGAAATCAAGGAAAGATGAGTAAATATCAACCTGTATC	2880
Db	2821	TTGAATGTGACAAAAAGGAAGAAATCAAGGAAAGATGAGTAAATATCAACCTGTATC	2880
Qy	2881	AGACAGTTAATATCACTGCAAGGCTTTCCTGTGTTGCTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGCAAGGCTTTCCTGTGTTGCTCAGAAAGATTAAGCCAGTTGATA	2940

D	2881	AGCAGCTTAATATCTACCTGACGGCTTCTCTGCTGGTGCAGAAAGATTAAGCCAGTTGATA	2944
Q	2941	ATGCCAAATGTGTGATTCAAAAGAGGCTCTAGTGTGTCCTATCATCTCAGTTCCAGAGCA	3000
D	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGTGTGTCCTATCATCTCAGTTCCAGAGCA	3000
Q	3001	ACGAAACTGGAATCTATTCTCCAAATTAACATGACCTTTTACAAAACCATATCTATAC	3066
D	3001	ACGAAACTGGAATCTATTCTCCAAATTAACATGACCTTTTACAAAACCATATCTATAC	3066
Q	3061	CACACATTTTCCCTCAAGTCATTTGTTAAACTTAAATAGAAAAATCGCTAGAGG	3120
D	3061	CACACATTTTCCCTCAAGTCATTTGTTAAACTTAAATAGAAAAATCGCTAGAGG	3120
Q	3121	AAAACCTTGGAGAACATTCATATGTCACCTGAAAGAAATGGGAAATGGAACATTTCCA	3180
D	3121	AAAACCTTGGAGAACATTCATATGTCACCTGAAAGAAATGGGAAATGGAACATTTCCA	3180
Q	3181	GTACAGTGAACAATTAAGCCGTATATACATTAAGAAAAATGTTTTAAAGAGCCAGCT	3240
D	3181	GTACAGTGAACAATTAAGCCGTATATACATTAAGAAAAATGTTTTAAAGAGCCAGCT	3240
Q	3241	CAAGCAATATTAAGAATAGCTCCAGTACTATATGAAGTGGCTCCAGTATATATGA	3300
D	3241	CAAGCAATATTAAGAATAGCTCCAGTACTATATGAAGTGGCTCCAGTATATATGA	3300
Q	3301	TAGTGTCCAGTATGATAAAACATTCACACACAACTAGTATGAAACAGAGGCCCAAAATGA	3360
D	3301	TAGTGTCCAGTATGATAAAACATTCACACACAACTAGTATGAAACAGAGGCCCAAAATGA	3360
Q	3361	ATGCTATGCTTAGATTAAGGGGTTTTGCACACTGAGGCTATATAACAAAGCTTCCCTGAA	3420
D	3361	ATGCTATGCTTAGATTAAGGGGTTTTGCACACTGAGGCTATATAACAAAGCTTCCCTGAA	3420
Q	3421	GTAAATGTAAACATTCCTGAAATATAAAGCAAAATATGAAGAATGATGTCAGACTGTA	3480
D	3421	GTAAATGTAAACATTCCTGAAATATAAAGCAAAATATGAAGAATGATGTCAGACTGTA	3480
Q	3481	ATACAGATTTTCTCCATATCTGATTTCAATTAACATTAAGACGCTATGGGAATATCTC	3540
D	3481	ATACAGATTTTCTCCATATCTGATTTCAATTAACATTAAGACGCTATGGGAATATCTC	3540
Q	3541	ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATTAAG	3600
D	3541	ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATTAAG	3600
Q	3601	AAGATACATGTTTTGCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTTACAAAAAGC	3660
D	3601	AAGATACATGTTTTGCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTTACAAAAAGC	3660
Q	3661	TCCAGAAAGGAGACCTTAGAGAGGAGTCCTAGCCCTTCAACCATACATTTGGCTCAGG	3720
D	3661	TCCAGAAAGGAGACCTTAGAGAGGAGTCCTAGCCCTTCAACCATACATTTGGCTCAGG	3720
Q	3721	GTACCGAAGAGGGGCCAAGAAATATGAGTCTCAGAAAGAACTTATCTAGTAGATG	3780
D	3721	GTACCGAAGAGGGGCCAAGAAATATGAGTCTCAGAAAGAACTTATCTAGTAGATG	3780
Q	3781	AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
D	3781	AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Q	3841	CTACATGAGCAATAGACCGTGTACACGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900
D	3841	CTACATGAGCAATAGACCGTGTGTCTACGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Q	3901	TATCATTTGAAGAATAGCTTAAATATGACTGTGAGTAAACAGGTAATATTTGGCAAGCATCTC	3960
D	3901	TATCATTTGAAGAATAGCTTAAATATGACTGTGAGTAAACAGGTAATATATTTGGCAAGCATCTC	3960
Q	3961	AGGAACATCACTTATAGTGAAGAAACAAATGTTCTGTAGCTGTTTTCTTCCACAGTGA	4020
D	3961	AGGAACATCACTTATAGTGAAGAAACAAATGTTCTGTAGCTGTTTTCTTCCACAGTGA	4020





Db 1 AGCTGCTGAGACTTCTGAGACCCCGCACAGGCTGTGGGGTTTCTCAAGTAATGCGCC 60  
Qy 61 CTTGGCTGAGAGGAGGCTTACCCCTGCTGCTGGTAAAGTTTCATTTGGAACAGAAAGAA 120  
Db 61 CTTGGCTGAGAGGAGGCTTACCCCTGCTGCTGGTAAAGTTTCATTTGGAACAGAAAGAA 120  
Qy 121 TGGATTTATCTGCTCTTCCGCTTGAAGAAATGTCATTAATGCTATGCGAGAAA 180  
Db 121 TGGATTTATCTGCTCTTCCGCTTGAAGAAATGTCATTAATGCTATGCGAGAAA 180  
Qy 181 TCTTGAAGTCCCATCTGCTGAGTGTATCAAGAGACCTGTCTCACAAAGTGTGACC 240  
Db 181 TCTTGAAGTCCCATCTGCTGAGTGTATCAAGAGACCTGTCTCACAAAGTGTGACC 240  
Qy 241 ACATATTTTGCAGAAATTTTGCATGCTGAGAACTTCTCAACGAGAAAGAGGCTTCACAGT 300  
Db 241 ACATATTTTGCAGAAATTTTGCATGCTGAGAACTTCTCAACGAGAAAGAGGCTTCACAGT 300  
Qy 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCTTACAGAAAGTATGAGATTAGTC 360  
Db 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCTTACAGAAAGTATGAGATTAGTC 360  
Qy 361 AACTGTGTAAGAGCTATGTAAGAAATCATTTGCTTTGAGTGTGACAGAGTTTGAAGT 420  
Db 361 AACTGTGTAAGAGCTATGTAAGAAATCATTTGCTTTGAGTGTGACAGAGTTTGAAGT 420  
Qy 421 ATGCAACAGCTATATATTTTGCAGAAAGAAATTAATCTCTCTGTAACATCTTAAAGATG 480  
Db 421 ATGCAACAGCTATATATTTTGCAGAAAGAAATTAATCTCTCTGTAACATCTTAAAGATG 480  
Qy 481 AAGTTTCTATCTCCAAAGATATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCTCCAAAGATATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCTCTCTCTGAGAGAAACCGTCTAGTCCAACTCTCTAACCTTGGAA 600  
Db 541 AACCCGAAATCTCTCTCTGAGAGAAACCGTCTAGTCCAACTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGAGAAAGAGCGGATACAACTCAAAAGAGCTGTCTTACATTG 660  
Db 601 CTGTGAGAACTCTGAGAGAAAGAGCGGATACAACTCAAAAGAGCTGTCTTACATTG 660  
Qy 661 AATGGAGATCTGATCTTCTGTAAGATACCGTTAATTAAGCAACTTCTGAGTGGGAG 720  
Db 661 AATGGAGATCTGATCTTCTGTAAGATACCGTTAATTAAGCAACTTCTGAGTGGGAG 720  
Qy 721 ATCAAGATTTGTTACAAATCACCCCTCAAGGAACCGAGATGAATCAGTTTGGATTCTG 780  
Db 721 ATCAAGATTTGTTACAAATCACCCCTCAAGGAACCGAGATGAATCAGTTTGGATTCTG 780  
Qy 781 CAAAAAGAGCTGCTGTAATTTCTGAGAGGATGTAACAAAATCTGACATCATCAAC 840  
Db 781 CAAAAAGAGCTGCTGTAATTTCTGAGAGGATGTAACAAAATCTGACATCATCAAC 840  
Qy 841 CCAGTAATATATGATTTGAACACCACTGAGAGAGCTGACACTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTAATATATGATTTGAACACCACTGAGAGAGCTGACACTGAGAGGATCCAGAAAGT 900  
Qy 901 ATCAGAGTATGCTGTTTCAAACTTGCATGTGAGAGCATGTGGCAAAATCTCATGCCA 960  
Db 901 ATCAGAGTATGCTGTTTCAAACTTGCATGTGAGAGCATGTGGCAAAATCTCATGCCA 960  
Qy 961 GCTCATTTACAGATGAGAACAGAGTTTATTAATCTCACTAAGAGCAAGATGATGAGAA 1020  
Db 961 GCTCATTTACAGATGAGAACAGAGTTTATTAATCTCACTAAGAGCAAGATGATGAGAA 1020  
Qy 1021 AGGCTGATTTCTGTAATAAAGCAAAAGAGCTGCTGCTTACAGAGAGGCAACATACAGAT 1080  
Db 1021 AGGCTGATTTCTGTAATAAAGCAAAAGAGCTGCTGCTTACAGAGAGGCAACATACAGAT 1080  
Qy 1081 GGGCTGTAAGTAAAGAAACATGTAATGATAGGCGAGCTCCAGACAGAAAGAAAGGTAG 1140  
Db 1081 GGGCTGTAAGTAAAGAAACATGTAATGATAGGCGAGACTCCAGACAGAAAGAAAGGTAG 1140

Qy 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTGATATCTGAAAGATGTTCCCTGGATTAACCTAATTAAGCAGATTCAGA 1260  
Db 1201 CAGAGAACTCTGATATCTGAAAGATGTTCCCTGGATTAACCTAATTAAGCAGATTCAGA 1260  
Qy 1261 AAGTTAATGATGTTTCCAGAAATGATGAACCTGTTAGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATGATGTTTCCAGAAATGATGAACCTGTTAGTTCTGATGACTCAATGATG 1320  
Qy 1321 GGGAGTCTGATCAATATGCCAAAGTACTGATGTAATTTGACGTTCTAATAGTATAGT 1380  
Db 1321 GGGAGTCTGATCAATATGCCAAAGTACTGATGTAATTTGACGTTCTAATAGTATAGT 1380  
Qy 1381 AATATTTGCTGTTCTGAGAAATATAGACTTACAGGAGATCCATGAGGCTTAA 1440  
Db 1381 AATATTTGCTGTTCTGAGAAATATAGACTTACAGGAGATCCATGAGGCTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGATTAATTTGAGACAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGATTAATTTGAGACAAATAT 1500  
Qy 1501 TTGGGAAACCTATGCGAAAGAGCAAGCCCTCCCACTTAAGCATGTAATGTAATATC 1560  
Db 1501 TTGGGAAACCTATGCGAAAGAGCAAGCCCTCCCACTTAAGCATGTAATGTAATATC 1560  
Qy 1561 TAATTTATGAGCACTTTTCTGAGCAAGATTAATTAAGAGAGGCTCCCTCAATA 1620  
Db 1561 TAATTTATGAGCACTTTTCTGAGCAAGATTAATTAAGAGAGGCTCCCTCAATA 1620  
Qy 1621 AATTAAGGCTAAAGAGAGCTTACATCAGAGCTTACCTGAGAGATTTTATCAAGAA 1680  
Db 1621 AATTAAGGCTAAAGAGAGCTTACATCAGAGCTTACCTGAGAGATTTTATCAAGAA 1680  
Qy 1681 CAGATTTGGCAGTTCAGAAAGCTCTGTAATGATTAATCAGGGAACCTAACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAGAAAGCTCTGTAATGATTAATCAGGGAACCTAACCAAGGAGC 1740  
Qy 1741 AGAATGCTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
Db 1741 AGAATGCTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
Qy 1801 CTATTCAGATGAGAAATATCTTAACCAATAGAACTCTGAGAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAATATCTTAACCAATAGAACTCTGAGAAAGAAATCTGCTTCA 1860  
Qy 1861 AAAGCAAGCTGACCTTAATTAAGCAGAGTATTAAGCAATATGGAATTAATTAATTC 1920  
Db 1861 AAAGCAAGCTGACCTTAATTAAGCAGAGTATTAAGCAATATGGAATTAATTAATTC 1920  
Qy 1921 ACAATTTCAAAAGCAGCTTAAGAAATAGGCTGAGAGGAGAACTTCTTACCAAGCATTC 1980  
Db 1921 ACAATTTCAAAAGCAGCTTAAGAAATAGGCTGAGAGGAGAACTTCTTACCAAGCATTC 1980  
Qy 1981 ATGCGCTGAACTAGTATCTAGTAAATCTTAAGCCCACTTAATTTGATGAAATTCGAA 2040  
Db 1981 ATGCGCTGAACTAGTATCTAGTAAATCTTAAGCCCACTTAATTTGATGAAATTCGAA 2040  
Qy 2041 TTGATAGTTGTTCTGAGAGTAAAGAAATTAAGAAATTAAGCAACCAATGCGAGTCA 2100  
Db 2041 TTGATAGTTGTTCTGAGAGTAAAGAAATTAAGAAATTAAGCAACCAATGCGAGTCA 2100  
Qy 2101 GGCACAGAGAAACCTTAACCTCATGGAAGGTAAAGAACTGCAACTGAGAGCCAAAGAGA 2160  
Db 2101 GGCACAGAGAAACCTTAACCTCATGGAAGGTAAAGAACTGCAACTGAGAGCCAAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGAGTAAAGAAATGATGAGAGAGTACTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGAGTAAAGAAATGATGAGAGAGTACTTCCAGAGCTGA 2220



QY	2221	AGTAAACAAATGACCCCTGGTCTTTTCTCTAATAGGTTCAATATACAGTGAATCTTAAGAT	2280
Db	2221	AGTTAAACAAATGACCCCTGGTCTTTTCTCTAATAGGTTCAATATACAGTGAATCTTAAGAT	2280
QY	2281	TTGTCAATCCGAGCCTTCCAAAGAAAGAAAACAGAAACTAGAAACAGTTAAAGGT	2340
Db	2281	TTGTCAATCCGAGCCTTCCAAAGAAAGAAAACAGAAACTAGAAACAGTTAAAGGT	2340
QY	2341	CTAATAATGCTGAAGACCCCAAAAGATCTCATGTTAAGTGAGAAAGGGTTTTCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAAAGATCTCATGTTAAGTGAGAAAGGGTTTTCAAACTG	2400
QY	2401	AAAAGATCTGTAGAGATGACAGATATTTCAATGTTACTGTTACTGATTAATGCGACTAGG	2460
Db	2401	AAAAGATCTGTAGAGATGACAGATATTTCAATGTTACTGTTACTGATTAATGCGACTAGG	2460
QY	2461	AAAGATATCTGTTCTCTGGAAGTTAGCACTCTAGGAAAGCAAAAACAGAACCAATAAT	2520
Db	2461	AAAGATATCTGTTCTCTGGAAGTTAGCACTCTAGGAAAGCAAAAACAGAACCAATAAT	2520
QY	2521	GTTGAGTCACTGTGCAAGATTTTGAAAACCCCAAGGAGCAATTCATGGTGTTCCAAG	2580
Db	2521	GTTGAGTCACTGTGCAAGATTTTGAAAACCCCAAGGAGCAATTCATGGTGTTCCAAG	2580
QY	2581	ATAATAGAAATGACACAGAAAGCCTTTAATGATTCATTTGGGACATGAATTAACCAAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGCCTTTAATGATTCATTTGGGACATGAATTAACCAAGTC	2640
QY	2641	GGGAAACACAGCATGAAATGGAAGAAAGTAATGATGCTCAGTATTTGGCAATACAT	2700
Db	2641	GGGAAACACAGCATGAAATGGAAGAAAGTAATGATGCTCAGTATTTGGCAATACAT	2700
QY	2701	TCAAGGTTTCAAAGCGCCAGCTCATTTGCTCTGTTTCAATCTCAGGAATGCAAGAGAG	2760
Db	2701	TCAAGGTTTCAAAGCGCCAGCTCATTTGCTCTGTTTCAATCTCAGGAATGCAAGAGAG	2760
QY	2761	AATGTGCAACATTTCTCTGCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGATGTGAACAAAGGAAGAAATCAAGGAAAGTAAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGATGTGAACAAAGGAAGAAATCAAGGAAAGTAAGTCTAATATCAAGCCTGTAC	2880
QY	2881	AGACAGTTAATATCATCGCAGCGCTTCTCTGTGGTTGTCAGAAAGATAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCATCGCAGCGCTTCTCTGTGGTTGTCAGAAAGATAAGCCAGTTGATA	2940
QY	2941	ATGCCAATGTAGTATTAAGAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAGAGSCA	3000
Db	2941	ATGCCAATGTAGTATTAAGAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAGAGSCA	3000
QY	3001	ACGAAACTGGACATATTAACACCAATTAACATGAGATTTTACAAAACCCATATCTGTATAC	3060
Db	3001	ACGAAACTGGACATATTAACACCAATTAACATGAGATTTTACAAAACCCATATCTGTATAC	3060
QY	3061	CACCACCTTTTCCCATCAATCTATTTGTTAAACCTAAATGTAGAAAAATCTGCTAGAG	3120
Db	3061	CACCACCTTTTCCCATCAATCTATTTGTTAAACCTAAATGTAGAAAAATCTGCTAGAG	3120
QY	3121	AAAACTTTGAGGAACATTCATATGTCACTGAGAAAGAAATGGGAAATGAGAACATTCOA	3180
Db	3121	AAAACTTTGAGGAACATTCATATGTCACTGAGAAAGAAATGGGAAATGAGAACATTCOA	3180
QY	3181	GTAACAGGAGACAAATTAAGCCGTAATTAACAATTGAGAAAATGTTTTTAAAGAGCCACT	3240
Db	3181	GTAACAGGAGACAAATTAAGCCGTAATTAACAATTGAGAAAATGTTTTTAAAGAGCCACT	3240
QY	3241	CAACCAATATTAATGAAGTATAGGTTTCCAGTACTATGAATGGGCTCCAGTATTAATGAA	3300
Db	3241	CAACCAATATTAATGAAGTATAGGTTTCCAGTACTATGAATGGGCTCCAGTATTAATGAA	3300
QY	3301	TAGGTTCCAGTATGATGAACAACTTCAAGCAGAACTAGTAGAACAAGAGGCCAAAATTTGA	3360

Dd	3301	TAGGTTCCAGTAGAATAATTCACGACGAACCTAGTGTGAACAAGAGGGCCAAAATTGCA	3360
Oy	3361	ATGCATATCCTTAAGTTATGGGGTTTTTGCAACTGAGGTCTATAAAAGAAGCTCTCCGGA	3420
Dd	3361	ATGCTATGCTTATAGTTATGGGGTTTTGCAACCTGASGTCTATAAAAGAAAGCTCTCTCGGA	3420
Oy	3421	GTAATTGTAAAGCATCTGAAATATAAAAAGCAAGATATGAAGAAAGTAGTACGACTGTTA	3480
Dd	3421	GTAATTGTAAAGCATCTGAAATATAAAAAGCAAGATATGAAGAAAGTAGTACGACTGTTA	3480
Oy	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTAACTTAACAAGCCTATGGAACTACTC	3540
Dd	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTAACTTAACAAGCCTATGGAACTACTC	3540
Oy	3541	ATGCATCTCAGGTTGTGTTCTGAGAACACCAGTATACCTGTTATGATGATGGTAAATPAAG	3600
Dd	3541	ATGCATCTCAGGTTGTGTTCTGAGAACACCAGTATACCTGTTATGATGATGGTAAATPAAG	3600
Oy	3601	AAGATACTAGTTTGTGTAATAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACGC	3660
Dd	3601	AAGATACTAGTTTGTGTAATAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACGC	3660
Oy	3661	TCCAGAAAGAGAGACTTAGCAGAGAGTCTTAGCCCTTTCACCATACATTTGGCTCAGG	3720
Dd	3661	TCCAGAGAGGAGACTTAGCAGAGAGTCTTAGCCCTTTCACCATACATTTGGCTCAGG	3720
Oy	3721	GTTACCGAAGAGGGGCCCAAAATTTAGAGTCCACAAAGAACTTATCTAGTGSAGATG	3780
Dd	3721	GTTACCGAAGAGGGGCCCAAAATTTAGAGTCCCTCAGAGAGAACTTATCTAGTGSAGATG	3780
Oy	3781	AAGAGCTCCCTGCTTCCAACACTGTATTGTTGTAAGTAAACAATATACCTTCTCAGT	3840
Dd	3781	AAGAGCTCCCTGCTTCCAACACTGTATTGTTGTAAGTAAACAATATACCTTCTCAGT	3840
Oy	3841	CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT	3900
Dd	3841	CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT	3900
Oy	3901	TATCATTTGAAGAAATAGSTTAAATGACTGCGAGTAACTAGTATTTGGCAAAGGATATC	3960
Dd	3901	TATCATTTGAAGAAATAGSTTAAATGACTGCGAGTAACTAGTATTTGGCAAAGGATATC	3960
Oy	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCACAGTSCA	4020
Dd	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCACAGTSCA	4020
Oy	4021	GTTGAATTGGAAAGACTTGACTGCAATACAAACCCAGAGATCCTTTCGTGATGGTCTT	4080
Dd	4021	GTTGAATTGGAAAGACTTGACTGCAATACAAACCCAGAGATCCTTTCGTGATGGTCTT	4080
Oy	4081	CCAAACAAATAGGCATCACTCTGAAAGCCAGGAGATGGTGTGAGTACAAAGAAATGG	4140
Dd	4081	CCAAACAAATAGGCATCACTCTGAAAGCCAGGAGATGGTGTGAGTACAAAGAAATGG	4140
Oy	4141	TTTTCAGATGATGAAGAAGAGAGAAAGGGGTTGGAGAAATATATACAAAGAGCAAAACA	4200
Dd	4141	TTTTCAGATGATGAAGAAGAGAGAAAGGGGTTGGAGAAATATATACAAAGAGCAAAACA	4200
Oy	4201	TGGATTTCAAACCTTAGTGAAGACGACATCTGGGTGTGAGAGTGAACCAAGCGTCTGAG	4260
Dd	4201	TGGATTTCAAACCTTAGTGAAGACGACATCTGGGTGTGAGAGTGAACCAAGCGTCTGAG	4260
Oy	4261	ACTGCTCAGGGCTATCTCTCACAAGTGAATTTTAAACCTAGCAGAGGGATPACATGAC	4320
Dd	4261	ACTGCTCAGGGCTATCTCTCACAAGTGAATTTTAAACCTAGCAGAGGGATPACATGAC	4320
Oy	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATTAAGACTGTGTTAGAACAGC	4380
Dd	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATTAAGACTGTGTTAGAACAGC	4380
Oy	4381	ATGGAGACCAAGCTTCTTAACAGCTTACCTTCATATAAGTACTCTTCTGCCCTGAGG	4440

D	4381	ATGGGAGCCAGCCTTCTACAGCTACCCCTTCATCATTAAGTACTCTTTCGCTTGAGG	4440
Q	4441	ACCTGGAAATCCAGAACAGACATCAGAAAAAGCAGTATTACTTCACGAAAAGTA	4500
D	4441	ACCTGGAAATCCAGAACAGACATCAGAAAAAGCAGTATTACTTCACGAAAAGTA	4500
Q	4501	GTGAATACCTATTAAGCCAAATCCAGAGCCTTCTGCTGACAACTTTGAGGTGTCTG	4560
D	4501	GTGAATACCTATTAAGCCAAATCCAGAGCCTTCTGCTGACAACTTTGAGGTGTCTG	4560
Q	4561	CAGATGTTCTACAGTAAAAATAAAGACAGAGTGGAAAAAGTCAATCCCTCTAAAT	4620
D	4561	CAGATGTTCTACAGTAAAAATAAAGACAGAGTGGAAAAAGTCAATCCCTCTAAAT	4620
Q	4621	GCCCATCATTAGATGATAGGTGGTACATGCACAGTTCCTGCGGAGTCTTCAGATAAGAA	4680
D	4621	GCCCATCATTAGATGATAGGTGGTACATGCACAGTTCCTGCGGAGTCTTCAGATAAGAA	4680
Q	4681	ACTACCATCTCAAGAGAGCTATTAAAGTTGTGATGTGGAGAGCAACAGCTGGAG	4740
D	4681	ACTACCATCTCAAGAGAGCTATTAAAGTTGTGATGTGGAGAGCAACAGCTGGAG	4740
Q	4741	AGTCTGGGCACACGATTTTACGAAAACTTTACTCTCCAAAGCAAGATCTACAGGAA	4800
D	4741	AGTCTGGGCACACGATTTTACGAAAACTTTACTCTCCAAAGCAAGATCTACAGGAA	4800
Q	4801	CCCCTTACCTGGAATCTGGAATCAGCCTCTCTCTGATGACCTGAAATCTGATCCTTCTG	4860
D	4801	CCCCTTACCTGGAATCTGGAATCAGCCTCTCTCTGATGACCTGAAATCTGATCCTTCTG	4860
Q	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAATACCATCTTCAACTCTGCATTTGA	4920
D	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAATACCATCTTCAACTCTGCATTTGA	4920
Q	4921	AAGTTCCCCAATGGAAGTGTGCAAAATCTCCAGAGTCCAGCGTGCATCACTACTG	4980
D	4921	AAGTTCCCCAATGGAAGTGTGCAAAATCTCCAGAGTCCAGCGTGCATCACTACTG	4980
Q	4981	ATACTGCTGGGTAAATGCAATGGAAGAAAGTGTGACAGAGGAGAAAGCCAGAAATTGACAG	5040
D	4981	ATACTGCTGGGTAAATGCAATGGAAGAAAGTGTGACAGAGGAGAAAGCCAGAAATTGACAG	5040
Q	5041	CTTCAACAGAAAGGGTCAACAAAAAGATGTCCATGGTGTCTGGCTCAACCCAGAG	5100
D	5041	CTTCAACAGAAAGGGTCAACAAAAAGATGTCCATGGTGTCTGGCTCAACCCAGAG	5100
Q	5101	AATTTATGCTCGTCAAGATTTGCCAGAAACACCATCACTTAACTAATCTAATTA	5160
D	5101	AATTTATGCTCGTCAAGATTTGCCAGAAACACCATCACTTAACTAATCTAATTA	5160
Q	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAAGTTGTGTGAACGGACAC	5220
D	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAAGTTGTGTGAACGGACAC	5220
Q	5221	TCAAAATATTTCTAGAGATTTGCCGGAGGAAAAATGGGTAGTACTATTTCTGGGTGACCC	5280
D	5221	TCAAAATATTTCTAGAGATTTGCCGGAGGAAAAATGGGTAGTACTATTTCTGGGTGACCC	5280
Q	5281	AGCTATTTAAAGAAAAAATCTGTAATAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
D	5281	AGCTATTTAAAGAAAAAATCTGTAATAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Q	5341	TCAATGGAAGAAACCCACAAAGTCCAAAGCGACAGAGATCCCAAGGACAGAAAGATCT	5400
D	5341	TCAATGGAAGAAACCCACAAAGTCCAAAGCGACAGAGATCCCAAGGACAGAAAGATCT	5400
Q	5401	TCAGGGGGCTAGAAATCTGTTGCTATAGGCGCTTCACAAACATGCCACAGATCAACTGG	5460
D	5401	TCAGGGGGCTAGAAATCTGTTGCTATAGGCGCTTCACAAACATGCCACAGATCAACTGG	5460
Q	5461	AATGATGTTACAGCTGTGTGGTGTCTGTGTGGTGAAGAGCTTTATCATTTACCTTGG	5520
D	5461	AATGATGTTACAGCTGTGTGGTGTCTGTGTGGTGAAGAGCTTTATCATTTACCTTGG	5520

OY	5521	GCACAGGTCCTCCACCCAATGTGGTTGTGTGACACCGCAGATGCCCTGGACACAGAGCAATGGCT	5580
Db	5521	GCACAGGTCCTCCACCCAATGTGGTTGTGTGACACCGCAGATGCCCTGGACACAGAGCAATGGCT	5580
OY	5581	TCCATGCAATTGGGAGAGATGTGTGAGGCACTGTGTGTGAACCCGAGAAGTGGGTGTGGACA	5640
Db	5581	TCCATGCAATTGGGAGAGATGTGTGAGGCACTGTGTGTGAACCCGAGAAGTGGGTGTGGACA	5640
OY	5641	GGTAGACACTCTACACAGTGCCAGAGGCTGGACACCTACTGTATATCCCCAGATCCCCACA	5700
Db	5641	GGTAGACACTCTACACAGTGCCAGAGGCTGGACACCTACTGTATATCCCCAGATCCCCACA	5700
OY	5701	GCCACTACTGA	5711
Db	5701	GCCACTACTGA	5711
RESULT 12			
AR007333	AR007333	5711 bp	DNA
LOCUS	Sequence 1 from patent US 5750400.	PAT	04-DEC-1998
DEFINITION	AR007333		
ACCESSION	93966817		
NID			
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 5711)		
	Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,		
	Schleifer,D.B. and Zeng,B.		
TITLE	Coding sequences of the human BRCA1 gene		
JOURNAL	Patent: US 5750400-A 1 12-MAY-1998;		
FEATURES	Location/Qualifiers		
source	1..5711		
BASE COUNT	1953 a 1099 c 1277 g 1382 t		
ORIGIN	/organism="unknown"		
<hr/>			
Query Match	99.8%; Score 5701.4; DB 6; Length 5711;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 5705; Conservative	0; Mismatches 6; Indels 0; Gaps 0;		
OY	1	AGCTGCGTAGAAGCTCCGCGAACCCCGCACAGGCTGTGGGTTTTCTCATTAAGTGGCC	60
Db	1	AGCTGCGTAGAAGCTCCGCGAACCCCGCACAGGCTGTGGGTTTTCTCATTAAGTGGCC	60
OY	61	CCTGGCGTCAGAGGCGCTTCACCTCTGCTGTGGTAAGTTCATTGGACAGAAAGAAA	120
Db	61	CCTGGCGTCAGAGGCGCTTCACCTCTGCTGTGGTAAGTTCATTGGACAGAAAGAAA	120
OY	121	TGGATTATCTGCTCTTGGCGTTGAAGAATCAAAATGTCATTATATCTTATGCGAAAA	180
Db	121	TGGATTATCTGCTCTTGGCGTTGAAGAATCAAAATGTCATTATATCTTATGCGAAAA	180
OY	181	TCTTAGAGTCCCATCTGCTGTGGATGATCAAGGAAGCTGTCTCCCAAAGTGTACC	240
Db	181	TCTTAGAGTCCCATCTGCTGTGGATGATCAAGGAAGCTGTCTCCCAAAGTGTGTACC	240
OY	241	ACATAATTTTGGCAAAATTTGCAATGCTGAACCTTCTCAACAGAAAGAGGGCTTCACAGT	300
Db	241	ACATAATTTTGGCAAAATTTGCAATGCTGAACCTTCTCAACAGAAAGAGGGCTTCACAGT	300
OY	301	GTCCTTTATGTAAGATATATTAACCAAAAGAGGCTCAAGAAAGTACGAGATTATATC	360
Db	301	GTCCTTTATGTAAGATATATTAACCAAAAGAGGCTCAAGAAAGTACGAGATTATATC	360
OY	361	AACCTGTGAAGAGCTATGAAATCAATTTMGCTTTCACCTTGACACAGATTGGAGT	420
Db	361	AACCTGTGAAGAGCTATGAAATCAATTTGTGCTTTCACCTTGACACAGATTGGAGT	420
OY	421	ATGCATAAGCTATATATTTTGCATAAAAGGAAATTAATCTCCGTGAACATGTAAAGATG	480

|||||  
Db 421 ATGCAAAAGCTATATATTTTGGAAAAAGAAAAATTAATCTCTCTTAACATCTTAAGAAATG 480  
Oy 481 AAGTTTCATCATCCAAAGATATGGGCTACAGAAACCGTGCCTCAAGAAAGCTTCTACAGAGTG 540  
Db 481 AAGTTTCATCATCCAAAGATATGGGCTACAGAAACCGTGCCTCAAGAAAGCTTCTACAGAGTG 540  
Oy 541 AACCCGAAAAATCCTTCTCTGCGAGAAACCACTCTCACTCTCTAACTTTGGA 600  
Db 541 AACCCGAAAAATCCTTCTCTGCGAGAAACCACTCTCACTCTCTAACTTTGGA 600  
Oy 601 CTGTGGAACCTGTGAGCAAGCAAGCGGATCAACCTCAAAAGAGTCTGTCAATTG 660  
Db 601 CTGTGGAACCTGTGAGCAAGCAAGCGGATCAACCTCAAAAGAGTCTGTCAATTG 660  
Oy 661 AATTGGAGTCGATCTTCTGAGATACCGTTAATAGGCAACTTATTCAGTGTGGAG 720  
Db 661 AATTGGAGTCGATCTTCTGAGATACCGTTAATAGGCAACTTATTCAGTGTGGAG 720  
Oy 721 ATCAGAATTTGTACAAATCACCCCTCAAGAACCAAGGAGTAAATCAGTTGATTCG 780  
Db 721 ATCAGAATTTGTACAAATCACCCCTCAAGAACCAAGGAGTAAATCAGTTGATTCG 780  
Oy 781 CAAAAAGGCTGCTGTGATTTTCTGAGACCGATGTAAACAAATCTGAACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGATTTTCTGAGACCGATGTAAACAAATCTGAACATCATCAAC 840  
Oy 841 CCAGTAATATATGATTGGAACACCACTGAGAAAGCGTGAAGCTGAGAGCATCCAGAAAGT 900  
Db 841 CCAGTAATATATGATTGGAACACCACTGAGAAAGCGTGAAGCTGAGAGCATCCAGAAAGT 900  
Oy 901 ATCAGGATGTTCTGTTCAAACTTGCAATGTGAGCCATGTGGCACAAAATCTCATGCCA 960  
Db 901 ATCAGGATGTTCTGTTCAAACTTGCAATGTGAGCCATGTGGCACAAAATCTCATGCCA 960  
Oy 961 GCTCATTTACAGATGAGAAAGCAAGCATTTATCTCATTAAGCAAGATGTGAGAAA 1020  
Db 961 GCTCATTTACAGATGAGAAAGCAAGCATTTATCTCATTAAGCAAGATGTGAGAAA 1020  
Oy 1021 AAGCTGAATTTCTGTATTAAGCAAAACAGCCCTGCTTAGCAAGAGCCAACTAACAGAT 1080  
Db 1021 AAGCTGAATTTCTGTATTAAGCAAAACAGCCCTGCTTAGCAAGAGCCAACTAACAGAT 1080  
Oy 1081 GGGCTGGAAGTAGAAACATGTATAGGGGAGCTCCAGCACAGAAAAAAAGTAG 1140  
Db 1081 GGGCTGGAAGTAGAAACATGTATAGGGGAGCTCCAGCACAGAAAAAAAGTAG 1140  
Oy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGAGAAACATGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGAGAAACATGCCATGCT 1200  
Oy 1201 CAGAGAACTCTGAGATACTGAAAGATGTTCTTGATTAACATAATAGCAGATTCAGA 1260  
Db 1201 CAGAGAACTCTGAGATACTGAAAGATGTTCTTGATTAACATAATAGCAGATTCAGA 1260  
Oy 1261 AAGTTAATGAGTGTTCCTCCAGAAAGTGAATCTTAGGTTCTGATGACTCATATGATG 1320  
Db 1261 AAGTTAATGAGTGTTCCTCCAGAAAGTGAATCTTAGGTTCTGATGACTCATATGATG 1320  
Oy 1321 GGGAGTCTGAATCAAAAGCAAGTAGCTGATGTTGAGAGCTTAAATAGAGTAGT 1380  
Db 1321 GGGAGTCTGAATCAAAAGCAAGTAGCTGATGTTGAGAGCTTAAATAGAGTAGT 1380  
Oy 1381 AATATTCGTCTTCTCAGAGAAATAGACTTACTGGCAGAGTATCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCGTCTTCTCAGAGAAATAGACTTACTGGCAGAGTATCTCATGAGGCTTTAA 1440  
Oy 1441 TATGTAAAGTAAAGAGTTCACCTCAATCAGTAGAGAGTAAATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTAAAGAGTTCACCTCAATCAGTAGAGAGTAAATTTGAAGCAAAATAT 1500  
Oy 1501 TTGGAAAAACCTATCGGAGAGAGGAGGAGGCTCCCAACTTAAGCATGTAAATATC 1560  
Db 1501 TTGGAAAAACCTATCGGAGAGAGGAGGAGGCTCCCAACTTAAGCATGTAAATATC 1560  
|||||  
Oy 1561 TAAATATAGAGACTTTTGTACTGAGCCACAGATTAATCAAGAGCTGCCCTCACAAATA 1620  
Db 1561 TAAATATAGAGACTTTTGTACTGAGCCACAGATTAATCAAGAGCTGCCCTCACAAATA 1620  
Oy 1621 AATTAAACCTTAAAGAGACTTATCATGAGCCCTTCACTCCCTGAGAGATTTTCAAGAAAG 1680  
Db 1621 AATTAAACCTTAAAGAGACTTATCATGAGCCCTTCACTCCCTGAGAGATTTTCAAGAAAG 1680  
Oy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAGAGAACTTAACAAAGAGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAGAGAACTTAACAAAGAGAGC 1740  
Oy 1741 AGAATGTCAGTGAATATATTAATTAAGTGTGTCATGAGATTAACAAAGAGTAT 1800  
Db 1741 AGAATGTCAGTGAATATATTAATTAAGTGTGTCATGAGATTAACAAAGAGTAT 1800  
Oy 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGATCTCTGAAAAAGAAATCTGTTCA 1860  
Db 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGATCTCTGAAAAAGAAATCTGTTCA 1860  
Oy 1861 AAAGGAAAGCTGAACCTTAAGCAGAGTATAGCAATATGGAATGGAATTAATATTC 1920  
Db 1861 AAAGGAAAGCTGAACCTTAAGCAGAGTATAGCAATATGGAATGGAATTAATATTC 1920  
Oy 1921 ACAATTTCAAAAGCACTTAAAAAGATAGCTGAGAGAGAGTCTTCTACAGCATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAAAAAGATAGCTGAGAGAGAGTCTTCTACAGCATATTC 1980  
Oy 1981 ATGGCTTGAACCTAGTACTGATGAGAAATCTAAGCCCACTAATTTGTAATTTGCAA 2040  
Db 1981 ATGGCTTGAACCTAGTACTGATGAGAAATCTAAGCCCACTAATTTGTAATTTGCAA 2040  
Oy 2041 TTGATAGTTCTTACAGAGTAAAGATTAAGAAAAAAATTAACCAACCAATGCGAGTCA 2100  
Db 2041 TTGATAGTTCTTACAGAGTAAAGATTAAGAAAAAAATTAACCAACCAATGCGAGTCA 2100  
Oy 2101 GGCACAGCAGAAACCTTACACTCATGGAAGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
Db 2101 GGCACAGCAGAAACCTTACACTCATGGAAGTAAAGAACTGCAACTGAGCCAGAAAGA 2160  
Oy 2161 GTAACAGCCAAATGAAACAGACAAAGTAAAGACATGACAGTACTTTCCAGAGCTGA 2220  
Db 2161 GTAACAGCCAAATGAAACAGACAAAGTAAAGACATGACAGTACTTTCCAGAGCTGA 2220  
Oy 2221 AGTTAACAATGACACCTGCTCTTTACTAGTGTCTCAATACCAAGTAAAGAT 2280  
Db 2221 AGTTAACAATGACACCTGCTCTTTACTAGTGTCTCAATACCAAGTAAAGAT 2280  
Oy 2281 TTGTCAATCTAGCCTTCCAGAGAGAAAAAGAGAACTAGAAACAGTTAAAGT 2340  
Db 2281 TTGTCAATCTAGCCTTCCAGAGAGAAAAAGAGAACTAGAAACAGTTAAAGT 2340  
Oy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTGCAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAAAGGTTTGCAACTG 2400  
Oy 2401 AAAGTCTGTAGAGTGAAGTATTTCAATGATGATACCTGATAGATTAAGGCACTGAG 2460  
Db 2401 AAAGTCTGTAGAGTGAAGTATTTCAATGATGATACCTGATAGATTAAGGCACTGAG 2460  
Oy 2461 AAAGTATCTGTTACTGTAAGTATAGCACTTAGGAGAAAGGCAAAACAGAACCAATAAT 2520  
Db 2461 AAAGTATCTGTTACTGTAAGTATAGCACTTAGGAGAAAGGCAAAACAGAACCAATAAT 2520  
Oy 2521 GTGTGAGTCACTGTGACAGATTTGAAAAACCCCAAGGAGCTAATTCATGTTGTTCAAAG 2580  
Db 2521 GTGTGAGTCACTGTGACAGATTTGAAAAACCCCAAGGAGCTAATTCATGTTGTTCAAAG 2580  
Oy 2581 ATAAATAGAAATGACACAGAAAGGCTTAAAGTATCAATTGGGAGCAGAAAGTTAACACAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGGCTTAAAGTATCAATTGGGAGCAGAAAGTTAACACAGTC 2640  
|||||

OY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATCCTCAGTATTTGTCAGAAATACAT 2700  
| | | | |  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATCCTCAGTATTTGTCAGAAATACAT 2700  
OY 2701 TCAAGCTTCAAAAGGCGCATTTGCTCTGTTTCAATCCAGAAATGCAAGAGAG 2760  
| | | | |  
Db 2701 TCAAGCTTCAAAAGGCGCATTTGCTCTGTTTCAATCCAGAAATGCAAGAGAG 2760  
OY 2761 AATGTCAACATTTCTGCGCCACTGCGGTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
| | | | |  
Db 2761 AATGTCAACATTTCTGCGCCACTGCGGTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
OY 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAGATGCTATATATCAAGCCGTATC 2880  
| | | | |  
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAGATGCTATATATCAAGCCGTATC 2880  
OY 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTTGGTCAGAAAGATTAAGCCAGTTGATA 2940  
| | | | |  
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTTGGTCAGAAAGATTAAGCCAGTTGATA 2940  
OY 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
| | | | |  
Db 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
OY 3001 ACGAAACTGGAATCTTACTTCCAAATTAACATGAGCTTTTACAAAACCATATCTGATAC 3060  
| | | | |  
Db 3001 ACGAAACTGGAATCTTACTTCCAAATTAACATGAGCTTTTACAAAACCATATCTGATAC 3060  
OY 3061 CACCACTTTTCCCATCAAGTATCTTGTAAACTAATGTAAAGAAATCTGCTAGAGG 3120  
| | | | |  
Db 3061 CACCACTTTTCCCATCAAGTATCTTGTAAACTAATGTAAAGAAATCTGCTAGAGG 3120  
OY 3121 AAAACTTTGAGAACATTCATCACTGACCTGAAAGAAATGGAAATGGAACATTTCCAA 3180  
| | | | |  
Db 3121 AAAACTTTGAGAACATTCATCACTGACCTGAAAGAAATGGAAATGGAACATTTCCAA 3180  
OY 3181 GTACAGTAGACATTTAGCCCTAATTAACATTAAGAGAAATTTTAAAGAACGACGT 3240  
| | | | |  
Db 3181 GTACAGTAGACATTTAGCCCTAATTAACATTAAGAGAAATTTTAAAGAACGACGT 3240  
OY 3241 CAACCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
| | | | |  
Db 3241 CAACCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
OY 3301 TAGGTTCCAGTGAAGAAACATTCAGAGAACTAGGTAGAAAAGAGGCGCCAAAATTGA 3360  
| | | | |  
Db 3301 TAGGTTCCAGTGAAGAAACATTCAGAGAACTAGGTAGAAAAGAGGCGCCAAAATTGA 3360  
OY 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACCTGAGGTCATTAACAAAGTCTTCTCGGAA 3420  
| | | | |  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACCTGAGGTCATTAACAAAGTCTTCTCGGAA 3420  
OY 3421 GTAATTGTAACATCTCTGAATTAATAAAGCAAGATATGAAGAGTAGTTAGACTGTTA 3480  
| | | | |  
Db 3421 GTAATTGTAACATCTCTGAATTAATAAAGCAAGATATGAAGAGTAGTTAGACTGTTA 3480  
OY 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTAAAGAGGCTATGGGAAGTAGTC 3540  
| | | | |  
Db 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTAAAGAGGCTATGGGAAGTAGTC 3540  
OY 3541 ATGATATCTCAGGTTTGTCTGAGACACTGATGACCTGTAGATATATGCTGAATTAAGG 3600  
| | | | |  
Db 3541 ATGATATCTCAGGTTTGTCTGAGACACTGATGACCTGTAGATATATGCTGAATTAAGG 3600  
OY 3601 AAGATAGTATGTTGCTGAATAATGACATTAAGGAAGTGTCTGTTTAAAGAGG 3660  
| | | | |  
Db 3601 AAGATAGTATGTTGCTGAATAATGACATTAAGGAAGTGTCTGTTTAAAGAGG 3660  
OY 3661 TCCAGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTACACCATACATTTGGCTCAGG 3720  
| | | | |  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTACACCATACATTTGGCTCAGG 3720

OY 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGACTTATCTAGTGAAGATG 3780  
| | | | |  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGACTTATCTAGTGAAGATG 3780  
OY 3781 AAGAGCTTCCCGCTCTCCAAACCTGTTATTTGGTAAAGTAAACATATATCTTCAGT 3840  
| | | | |  
Db 3781 AAGAGCTTCCCGCTCTCCAAACCTGTTATTTGGTAAAGTAAACATATATCTTCAGT 3840  
OY 3841 CTACTAGGCATAGCACCGCTTCTACCGAGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
| | | | |  
Db 3841 CTACTAGGCATAGCACCGCTTCTACCGAGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
OY 3901 TATCATTAAGAAATAGCTTAATATGATGAGTAAACAGATATTTGGCAAGGATCTC 3960  
| | | | |  
Db 3901 TATCATTAAGAAATAGCTTAATATGATGAGTAAACAGATATTTGGCAAGGATCTC 3960  
OY 3961 AGGAACATCACCTTAGTAGAGAAACAAATTTTGTAGCTTGTCTTTCACAGTGA 4020  
| | | | |  
Db 3961 AGGAACATCACCTTAGTAGAGAAACAAATTTTGTAGCTTGTCTTTCACAGTGA 4020  
OY 4021 GTGAATTTGAAGAGCTTGAATCAATACAAACACCCAGATCTTCTTGTATGTTCTT 4080  
| | | | |  
Db 4021 GTGAATTTGAAGAGCTTGAATCAATACAAACACCCAGATCTTCTTGTATGTTCTT 4080  
OY 4081 CCAACCAATGAGGCTATCAGTCTGAAGCCAGGAGTGTGCTGAGTGAACAAAGATTTG 4140  
| | | | |  
Db 4081 CCAACCAATGAGGCTATCAGTCTGAAGCCAGGAGTGTGCTGAGTGAACAAAGATTTG 4140  
OY 4141 TTTTCAGATGTAAGAAAGAGAGAGGAGGCTTGAAGAAATTAATCAAGAGACAAAGCA 4200  
| | | | |  
Db 4141 TTTTCAGATGTAAGAAAGAGAGAGGAGGCTTGAAGAAATTAATCAAGAGACAAAGCA 4200  
OY 4201 TGGATTTCAACTTAAGTGAAGAGAGGAGGCTTGAAGAAATTAATCAAGAGAGGAG 4260  
| | | | |  
Db 4201 TGGATTTCAACTTAAGTGAAGAGAGGAGGCTTGAAGAAATTAATCAAGAGAGGAG 4260  
OY 4261 ACTGCTCAGGCTATCTCTCAGAGTACATTTTAACCACTCAGCAGAGGAGATACATG 4320  
| | | | |  
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTACATTTTAACCACTCAGCAGAGGAGATACATG 4320  
OY 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGCGTGAATCAAGAGCTGTGTGAACAC 4380  
| | | | |  
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGCGTGAATCAAGAGCTGTGTGAACAC 4380  
OY 4381 ATGGAGCCAGCCTTCTTAACAGTACCTTCATCAATAGTGAATCTTCTGCTTGAAG 4440  
| | | | |  
Db 4381 ATGGAGCCAGCCTTCTTAACAGTACCTTCATCAATAGTGAATCTTCTGCTTGAAG 4440  
OY 4441 ACCTGCGAAATCCAGAAACAAAGCAGATCAGAAAAAGAGATTAATCTCACAGAAAAAGTA 4500  
| | | | |  
Db 4441 ACCTGCGAAATCCAGAAACAAAGCAGATCAGAAAAAGAGATTAATCTCACAGAAAAAGTA 4500  
OY 4501 GTGAATACCTTAATGAAGCAGAAATCCAGAGAGGCTTCTGCTGCAAGTTGAGGTCTG 4560  
| | | | |  
Db 4501 GTGAATACCTTAATGAAGCAGAAATCCAGAGAGGCTTCTGCTGCAAGTTGAGGTCTG 4560  
OY 4561 CAGATAGTCTTACAGTAAAAATTAAGAACACAGAGTGAAGAGTCACTCCCTCTTAAT 4620  
| | | | |  
Db 4561 CAGATAGTCTTACAGTAAAAATTAAGAACACAGAGTGAAGAGTCACTCCCTCTTAAT 4620  
OY 4621 GCCCATATTTAGATAGATAGGTGTACATGCAAGTTGCTTGGGAGTCTTCAAAATAGAA 4680  
| | | | |  
Db 4621 GCCCATATTTAGATAGATAGGTGTACATGCAAGTTGCTTGGGAGTCTTCAAAATAGAA 4680  
OY 4681 ACTACCATCTCAAGAGAGAGTCAATTAAGTTGTGATGTGAGAGAGCAACAGCTGAAG 4740  
| | | | |  
Db 4681 ACTACCATCTCAAGAGAGAGTCAATTAAGTTGTGATGTGAGAGAGCAACAGCTGAAG 4740  
OY 4741 AGTCTGGGCCACAGATTTGAACGAAACATCTTACTTGGCAGAGGCAAGTCTAGAGGGA 4800  
| | | | |  
Db 4741 AGTCTGGGCCACAGATTTGAACGAAACATCTTACTTGGCAGAGGCAAGTCTAGAGGGA 4800  
OY 4801 CCCCTTACCTGGAAATCTGGAATACAGCCTCTTCTGTATACCTGAAATCTGATCTTCTG 4860  
| | | | |



QY 841 CCAATTAATGATTTGACACCACTGGAAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT 900  
DB 841 CCAATTAATGATTTGACACCACTGGAAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT 900  
QY 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAACAATACTCATGCCA 960  
DB 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAACAATACTCATGCCA 960  
QY 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTACTTAAGACAGAAATGAATGTAGAA 1020  
DB 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTACTTAAGACAGAAATGAATGTAGAA 1020  
QY 1021 AGGCTGAATCTGTAATTAAGCAAAAGCGCTGCTGAGAGGCAACAATATCAAT 1080  
DB 1021 AGGCTGAATCTGTAATTAAGCAAAAGCGCTGCTGAGAGGCAACAATATCAAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGCGGACTCCAGCAGCAAAAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGCGGACTCCAGCAGCAAAAAAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAGCAAACTGCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAGCAAACTGCCATGCT 1200  
QY 1201 CAGAGATCCTAGAGATCTGAGAAATGTTCTTGATACACTTAATAGCAGCATTCAGA 1260  
DB 1201 CAGAGATCCTAGAGATCTGAGAAATGTTCTTGATACACTTAATAGCAGCATTCAGA 1260  
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGTGTGAACTGTGAGTTCTGATGACTCAGATGATG 1320  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGTGTGAACTGTGAGTTCTGATGACTCAGATGATG 1320  
QY 1321 GGGAGTCTGATCAATCAATGCCAAGTAGTGATGTAATGAGCTTCAATAGAGTAGATG 1380  
DB 1321 GGGAGTCTGATCAATCAATGCCAAGTAGTGATGTAATGAGCTTCAATAGAGTAGATG 1380  
QY 1381 AATATTCTGCTTCTTCAGAGAAATAGACTACTGGCAGAGTACCTCATAGGCTTTAA 1440  
DB 1381 AATATTCTGCTTCTTCAGAGAAATAGACTACTGGCAGAGTACCTCATAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAAGTCTCACTCAAACTAGTAGAGAGTAAATATTGGAACAATAAT 1500  
DB 1441 TATGTAAAGTGAAGAAGTCTCACTCAAACTAGTAGAGAGTAAATATTGGAACAATAAT 1500  
QY 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCACTTAAGCAGATGTAAGTGAATC 1560  
DB 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCACTTAAGCAGATGTAAGTGAATC 1560  
QY 1561 TAATTAAGAGCATTTGTTACTAGGCCACAGATATACAGAGAGTCCCTCCCAATA 1620  
DB 1561 TAATTAAGAGCATTTGTTACTAGGCCACAGATATACAGAGAGTCCCTCCCAATA 1620  
QY 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCCCTTCACTCCTGAGAGATTTTATCAAGAA 1680  
DB 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCCCTTCACTCCTGAGAGATTTTATCAAGAA 1680  
QY 1681 CAGATTGGGAGTTTCAAAAAGACTCTGAATGATTAATCAGGGAATTAACCAAGGAGC 1740  
DB 1681 CAGATTGGGAGTTTCAAAAAGACTCTGAATGATTAATCAGGGAATTAACCAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATATTACTAATAGTGTGATGAGAAATTAACCAAGGATTT 1800  
DB 1741 AGAATGCTCAAGTGAATATTACTAATAGTGTGATGAGAAATTAACCAAGGATTT 1800  
QY 1801 CATTTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTCTTTCA 1860  
DB 1801 CATTTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTCTTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTATTAAGCAGAGTATAGCAATATGGAATTAATTAATTC 1920  
DB 1861 AAACGAAAGCTGAACCTATTAAGCAGAGTATAGCAATATGGAATTAATTAATTC 1920  
QY 1921 ACAATTCAAAAGCACTTAACCAATAGAGTGTGAGAGAAAGTCTTCAACAGGATATTC 1980  
DB 1921 ACAATTCAAAAGCACTTAACCAATAGAGTGTGAGAGAAAGTCTTCAACAGGATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTAGTGAATGAATCTAAGCCACCTAATGTACTGAATTTGCAAA 2040  
DB 1981 ATGCGCTTGAACCTAGTAGTGAATGAATCTAAGCCACCTAATGTACTGAATTTGCAAA 2040  
QY 2041 TTGATAGTGTGTTTCAAGAGTGAAGATTAAGAAAAAAGTAACAACCAATGCCAGTCA 2100  
DB 2041 TTGATAGTGTGTTTCAAGAGTGAAGATTAAGAAAAAAGTAACAACCAATGCCAGTCA 2100  
QY 2101 GGCACAGAGAAACCTCAACTCATGGAAGTAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGA 2160  
DB 2101 GGCACAGAGAAACCTCAACTCATGGAAGTAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGA 2160  
QY 2161 GTAACAGCCCAATGAACAGACAAAGTAAAGAGATGACAGCATGTTTCCAGAGCTGA 2220  
DB 2161 GTAACAGCCCAATGAACAGACAAAGTAAAGAGATGACAGCATGTTTCCAGAGCTGA 2220  
QY 2221 AGTTAACAATGACACTGTGTTTCTTACTAAGTGTCAATACAGTGAATTAAGAAAT 2280  
DB 2221 AGTTAACAATGACACTGTGTTTCTTACTAAGTGTCAATACAGTGAATTAAGAAAT 2280  
QY 2281 TTGTCAATCCTAGCCTTCCAAAGAAAGAAAGAAAGAAAGTGAAGTGAAGTGAAGTGA 2340  
DB 2281 TTGTCAATCCTAGCCTTCCAAAGAAAGAAAGAAAGAAAGTGAAGTGAAGTGAAGTGA 2340  
QY 2341 CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAGTGAAGTGAAGTGA 2400  
DB 2341 CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAGTGAAGTGAAGTGA 2400  
QY 2401 AAGATCTGTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2460  
DB 2401 AAGATCTGTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2460  
QY 2461 AAGATCTGTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2520  
DB 2461 AAGATCTGTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2520  
QY 2521 GTGTAGTCAAGTGTGACAGATTTTGAAGAACCCCAAGGAGTCAATTCAGTGTGTTCCAA 2580  
DB 2521 GTGTAGTCAAGTGTGACAGATTTTGAAGAACCCCAAGGAGTCAATTCAGTGTGTTCCAA 2580  
QY 2581 ATTAATGAATGACACAGAAAGCTTTAAGTATCATGTTGGAGATGAGTGAACACAGT 2640  
DB 2581 ATTAATGAATGACACAGAAAGCTTTAAGTATCATGTTGGAGATGAGTGAACACAGT 2640  
QY 2641 GGGAAACAGCATGAAGAAATGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
DB 2641 GGGAAACAGCATGAAGAAATGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
QY 2701 TCAAGTTTCAAAAGCGGCACTTTGCTGTGTTTCAATCCAGAAATGAGAAAGG 2760  
DB 2701 TCAAGTTTCAAAAGCGGCACTTTGCTGTGTTTCAATCCAGAAATGAGAAAGG 2760  
QY 2761 AATGTGCAATTTCTGCCCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAGGCTACTT 2820  
DB 2761 AATGTGCAATTTCTGCCCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAGGCTACTT 2820  
QY 2821 TTGAATGTAAGAAAGGAAAGAAATCAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2880  
DB 2821 TTGAATGTAAGAAAGGAAAGAAATCAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2880  
QY 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTGTTGTTGAGAAAGTGAAGTGAAGTGAAGT 2940  
DB 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTGTTGTTGAGAAAGTGAAGTGAAGTGAAGT 2940  
QY 2941 ATGCCAAATGATATCAAGAGAGGCTGTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000  
DB 2941 ATGCCAAATGATATCAAGAGAGGCTGTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000  
QY 3001 ACGAACTGAGCTCATTAATCCAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3060  
DB 3001 ACGAACTGAGCTCATTAATCCAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3060



```
Db 3001 ACGAACTGGACTCATTTACTCCAAATTAACATGACTTTTACAAAACCCATATCTGATAC 3060
QY 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAACTAAATGTAAGAAAATCTGTAAGG 3120
Db 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAACTAAATGTAAGAAAATCTGTAAGG 3120
QY 3121 AAAACTTGGAGAACATTCATGATCAGCTGTAAGAGAAATGGAAATGAGACATTCCAA 3180
Db 3121 AAAACTTGGAGAACATTCATGATCAGCTGTAAGAGAAATGGAAATGAGACATTCCAA 3180
QY 3181 GTACAGTGAACAAATTAAGCCGTAATACATTAAGAGAAATGTTTTAAAGAACCAAGCT 3240
Db 3181 GTACAGTGAACAAATTAAGCCGTAATACATTAAGAGAAATGTTTTAAAGAACCAAGCT 3240
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAGTGGGCTCCAGTATTATGAAA 3300
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAGTGGGCTCCAGTATTATGAAA 3300
QY 3301 TAGTTCAGATGATGAAGAACATTCAGAGACTAGGTAGAAAACAGAGGCCAAATTGA 3360
Db 3301 TAGTTCAGATGATGAAGAACATTCAGAGACTAGGTAGAAAACAGAGGCCAAATTGA 3360
QY 3361 ATGCTATGCTTAATTAAGGGGTTTGCAACCTGAGGCTATTAACAAGCTTCCTGSA 3420
Db 3361 ATGCTATGCTTAATTAAGGGGTTTGCAACCTGAGGCTATTAACAAGCTTCCTGSA 3420
QY 3421 GTAATTGTAAGATCCTGAAATAAAAAGCAAGATATGAAGAAGTAGTTACAGACTGTT 3480
Db 3421 GTAATTGTAAGATCCTGAAATAAAAAGCAAGATATGAAGAAGTAGTTACAGACTGTT 3480
QY 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTACAGACCTATGGAGAGTAGTC 3540
Db 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTACAGACCTATGGAGAGTAGTC 3540
QY 3541 ATACATCTCGGTTTGTCTGAGACACCTGATACCGTTAGATGATGGTGAATTAAG 3600
Db 3541 ATACATCTCGGTTTGTCTGAGACACCTGATACCGTTAGATGATGGTGAATTAAG 3600
QY 3601 AAGATACTAGTTTGTGTAAGATGACATTAAGGAAATTCCTGTTTATGACAAAAGC 3660
Db 3601 AAGATACTAGTTTGTGTAAGATGACATTAAGGAAATTCCTGTTTATGACAAAAGC 3660
QY 3661 TCCAGAAAGAGAGCTTAGAGAGAGTCTTAGCCCTTACACCATTAACATTTGGCTCAG 3720
Db 3661 TCCAGAAAGAGAGCTTAGAGAGAGTCTTAGCCCTTACACCATTAACATTTGGCTCAG 3720
QY 3721 GTTACGGAAGAGGGGCCAAGAAATTAAGTCTCAGAGAGAACTATCTAGTGAAGATG 3780
Db 3721 GTTACGGAAGAGGGGCCAAGAAATTAAGTCTCAGAGAGAACTATCTAGTGAAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840
QY 3841 CTACTAGGATAGACACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTA 3900
Db 3841 CTACTAGGATAGACACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTA 3900
QY 3901 TATCATTTGAAGATTAAGTAAATGACTGACAGTAAACAGGTAATTTGGCAAGGACATCT 3960
Db 3901 TATCATTTGAAGATTAAGTAAATGACTGACAGTAAACAGGTAATTTGGCAAGGACATCT 3960
QY 3961 AGGACATCACTTAAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCACAGTGA 4020
Db 3961 AGGACATCACTTAAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCACAGTGA 4020
QY 4021 GTGAATTTGAAGCTGATCGCAAAATACAAACCCAGAGATCCTTTCTGATTTGTTCTT 4080
Db 4021 GTGAATTTGAAGCTGATCGCAAAATACAAACCCAGAGATCCTTTCTGATTTGTTCTT 4080
QY 4081 CCAAAACAAATGAAGCATAGTGTGAAGAGCCAGAGAGTGGTGTGATGACAAAGAAATGG 4140
Db 4081 CCAAAACAAATGAAGCATAGTGTGAAGAGCCAGAGAGTGGTGTGATGACAAAGAAATGG 4140

QY 4141 TTTCAGATGATGAAGAAAGAGAACGGGCTTGGAAGAAAAATATCAAGAGACAAAGCA 4200
Db 4141 TTTCAGATGATGAAGAAAGAGAACGGGCTTGGAAGAAAAATATCAAGAGAGCAAAAGCA 4200
QY 4201 TGGATTCAAACCTTAAGTGAAGACGATCTGGGTGTGAGAGTGAACACGCTCTGGAAG 4260
Db 4201 TGGATTCAAACCTTAAGTGAAGACGATCTGGGTGTGAGAGTGAACACGCTCTGGAAG 4260
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGAGTACATTTTAACCACTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGAGTACATTTTAACCACTCAGCAGAGGATACCATGC 4320
QY 4321 AACATACCTGATTAAGCTCCAGCAGAGAAATGGCTGAAGTGTGTTAAGAACAC 4380
Db 4321 AACATACCTGATTAAGCTCCAGCAGAGAAATGGCTGAAGTGTGTTAAGAACAC 4380
QY 4381 ATGGAGCCAGGCTTTAAGCAGCTACCTTCCATCTAAGTACTCTTGTCCCTTGAGG 4440
Db 4381 ATGGAGCCAGGCTTTAAGCAGCTACCTTCCATCTAAGTACTCTTGTCCCTTGAGG 4440
QY 4441 ACCTGCAATCCAGAACAAAGACATCAGAAAAGCAGTATTAACTTACAGAAAAGTA 4500
Db 4441 ACCTGCAATCCAGAACAAAGACATCAGAAAAGCAGTATTAACTTACAGAAAAGTA 4500
QY 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGCAAGTGTGAGGTCTG 4560
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGCAAGTGTGAGGTCTG 4560
QY 4561 CAGATAGTTCTACAGTAAAAATTAAGAACAGAGAGTGAAGAGTATCCCTTCTAAT 4620
Db 4561 CAGATAGTTCTACAGTAAAAATTAAGAACAGAGAGTGAAGAGTATCCCTTCTAAT 4620
QY 4621 GCCATCATTAAGTATGATGAGTGTGATCAGAGTGTCTGAGAGTCTTCAAGTAAGAA 4680
Db 4621 GCCATCATTAAGTATGATGAGTGTGATCAGAGTGTCTGAGAGTCTTCAAGTAAGAA 4680
QY 4681 ACTACCATCTCAGAGAGGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAAG 4740
Db 4681 ACTACCATCTCAGAGAGGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAAG 4740
QY 4741 AGTCTGGGCCACAGATTTGACAGGAAACATCTTACTTGCAGAGGCAAGATCTAGAGGGA 4800
Db 4741 AGTCTGGGCCACAGATTTGACAGGAAACATCTTACTTGCAGAGGCAAGATCTAGAGGGA 4800
QY 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTCTGATGATACCTGGAATCTGATCTCTG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTCTGATGATACCTGGAATCTGATCTCTG 4860
QY 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTGGCAACATACCATCTTCACCTGATGA 4920
Db 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTGGCAACATACCATCTTCACCTGATGA 4920
QY 4921 AAGTTCGCCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980
Db 4921 AAGTTCGCCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980
QY 4981 ATACTGCTGGGTATATGATGAAAGAAAGTGTGAGAGGGAAGCCAGAAATGACAG 5040
Db 4981 ATACTGCTGGGTATATGATGAAAGAAAGTGTGAGAGGGAAGCCAGAAATGACAG 5040
QY 5041 CTTCAACAGAAAAGGCTCAACAAAAGATGTCATGGTGTCTGGCTGACCCCGAGAG 5100
Db 5041 CTTCAACAGAAAAGGCTCAACAAAAGATGTCATGGTGTCTGGCTGACCCCGAGAG 5100
QY 5101 AATTTATGCTGTGTGTAAGTGTGCAAGAAAACACACATCACTTAACTAATCTAATTA 5160
Db 5101 AATTTATGCTGTGTGTAAGTGTGCAAGAAAACACACATCACTTAACTAATCTAATTA 5160
QY 5161 CTGAAGAGACTACTATGTTGTTATGAAGAACAGATGCTAGTGTGTGAGAGGAGAC 5220
Db 5161 CTGAAGAGACTACTATGTTGTTATGAAGAACAGATGCTAGTGTGTGAGAGGAGAC 5220
```

QY 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGTAGTTAGTATTTCTGGGTGACC 5280  
|||||  
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGTAGTTAGTATTTCTGGGTGACC 5280  
QY 5281 AGCTCTTTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTACAGAGAGATGTGG 5340  
|||||  
Db 5281 AGCTCTTTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTACAGAGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACACCAAGGTCACCAAGGAGCAGAGAGATCCAGAGAGAAAGATCT 5400  
|||||  
Db 5341 TCAATGGAAGAAACACCAAGGTCACCAAGGAGCAGAGAGATCCAGAGAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTCCACCAATGCTCCAGAGATTAAGTGG 5460  
|||||  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTCCACCAATGCTCCAGAGATTAAGTGG 5460  
QY 5461 AATGATGATGACAGCTGTGTGCTCTGTGTGGAAGAGAGCTTTCATCATTCACCTTG 5520  
|||||  
Db 5461 AATGATGATGACAGCTGTGTGCTCTGTGTGGAAGAGAGCTTTCATCATTCACCTTG 5520  
QY 5521 GCACAGGTGTCACCCAAATGTGTGTGTGACAGCCAGATGCTGACAGAGAGCAATGGCT 5580  
|||||  
Db 5521 GCACAGGTGTCACCCAAATGTGTGTGTGACAGCCAGATGCTGACAGAGAGCAATGGCT 5580  
QY 5581 TCCATGCAATGGGAGATGTGTGAGGACCTGTGTGACCCGAGATGGGTGTGGACA 5640  
|||||  
Db 5581 TCCATGCAATGGGAGATGTGTGAGGACCTGTGTGACCCGAGATGGGTGTGGACA 5640  
QY 5641 GTGTAGCACTCTACAGTGGCAGAGGTGAGACACTACATACCCAGATCCGCCACA 5700  
|||||  
Db 5641 GTGTAGCACTCTACAGTGGCAGAGGTGAGACACTACATACCCAGATCCGCCACA 5700  
QY 5701 GCCACTACTGA 5711  
|||||  
Db 5701 GCCACTACTGA 5711  
REFERENCE 14  
LOCUS 140803 5712 bp DNA PAT 01-MAY-1997  
DEFINITION Sequence 12 from patent US 5622829.  
ACCESSION 140803  
NID 92082283  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS King, M., Friedmann, L., Ostermeyer, B., Rowell, S., Lynch, E., Szabo, C.  
TITLE Genetic markers for breast, ovarian, and prostatic cancer  
JOURNAL Patent: US 5622829-A 12 22-APR-1997;  
FEATURES Location/Qualifiers  
source 1..5712  
BASE COUNT 1957 a 1099 c 1274 g 1382 t  
ORIGIN  
Query Match 99.8%; Score 5698.4; DB 6; Length 5712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 1; gaps 1;

Db 121 TGAATTTATCTGCTCTTCGCGTTGAAGAGTACAAAATGCTATTATGCTATGACAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCCACAAAGTGTACC 240  
|||||  
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCCACAAAGTGTACC 240  
QY 241 ACATATTTTGAATTTTGCATGCTGAACCTTCTCAACGAGAAAGAGGCTTACAGT 300  
|||||  
Db 241 ACATATTTTGAATTTTGCATGCTGAACCTTCTCAACGAGAAAGAGGCTTACAGT 300  
QY 301 GTCTTTATGTAAGATGATATACCAAGAGAGCTTACAAAGAAAGTACGAGATTTAGTC 360  
|||||  
Db 301 GTCTTTATGTAAGATGATATACCAAGAGAGCTTACAAAGAAAGTACGAGATTTAGTC 360  
QY 361 AACTGTTGAAGAGCTATTGAAAATCATTTGTCTTTGAGCTTGACACAGTTTGGAGT 420  
|||||  
Db 361 AACTGTTGAAGAGCTATTGAAAATCATTTGTCTTTGAGCTTGACACAGTTTGGAGT 420  
QY 421 ATGCAAAAGCTTAAATTTTGCAAAAAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
|||||  
Db 421 ATGCAAAAGCTTAAATTTTGCAAAAAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
QY 481 AAGTTCTATCATCAAAAGTATGGCTACAGAAACCGTSCAAAAGACTTCTACAGAGTG 540  
|||||  
Db 481 AAGTTCTATCATCAAAAGTATGGCTACAGAAACCGTSCAAAAGACTTCTACAGAGTG 540  
QY 541 AACCCGAAAATCTCTCTTGCAGGAAACCAAGTCTCACTGCTCTTAACCTTGGAA 600  
|||||  
Db 541 AACCCGAAAATCTCTCTTGCAGGAAACCAAGTCTCACTGCTCTTAACCTTGGAA 600  
QY 601 CTGTGAACTCTGAGAACAAAGCAGCGATCAACCTCAAAAAGGCTGTCTACATTTG 660  
|||||  
Db 601 CTGTGAACTCTGAGAACAAAGCAGCGATCAACCTCAAAAAGGCTGTCTACATTTG 660  
QY 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATAGCAATTATTCAGTGTGGAG 720  
|||||  
Db 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATAGCAATTATTCAGTGTGGAG 720  
QY 721 ATCAAGATTTGTTACAAATCACCCTCAAGGAAACCAAGGATTAATCAGTTTGTG 780  
|||||  
Db 721 ATCAAGATTTGTTACAAATCACCCTCAAGGAAACCAAGGATTAATCAGTTTGTG 780  
QY 781 CAAAAAAGGCTGTGTAATTTCTGAGAGGATGTAACAATCTGACATCATCAAC 840  
|||||  
Db 781 CAAAAAAGGCTGTGTAATTTCTGAGAGGATGTAACAATCTGACATCATCAAC 840  
QY 841 CCAATATATATGATTTGAACACCACTGAGAACGCTGACAGCTGAGAGGATCCAGAAAAGT 900  
|||||  
Db 841 CCAATATATATGATTTGAACACCACTGAGAACGCTGAGAGGATCCAGAAAAGT 900  
QY 901 ATCAGGATGCTGTGTTTCAAACTTGACATGTGAGCATGTGGCAAAATACTATGCCA 960  
|||||  
Db 901 ATCAGGATGCTGTGTTTCAAACTTGACATGTGAGCATGTGGCAAAATACTATGCCA 960  
QY 961 GCTCATTTACAGATGAGAACAGCATGATTAATGATAGGCGGATCCCGACACAAAAAGGTAG 1140  
|||||  
Db 961 GCTCATTTACAGATGAGAACAGCATGATTAATGATAGGCGGATCCCGACACAAAAAGGTAG 1140  
QY 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGATGGAATTAAGCAAGAACTGCATGCT 1200  
|||||  
Db 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGATGGAATTAAGCAAGAACTGCATGCT 1200  
QY 1201 CAGAGATCTCTAGAGATGATGAAAGTGTCTTGTGATTAACATAATAGCAGATTGCA 1260  
|||||  
Db 1201 CAGAGATCTCTAGAGATGATGAAAGTGTCTTGTGATTAACATAATAGCAGATTGCA 1260

QY 1261 AAGTAAATGAGTGGTTTCCAGAAAGTATGATGACTGTAGGTTGATGACTACATGATG 1320  
DB 1261 AAGTAAATGAGTGGTTTCCAGAAAGTATGATGACTGTAGGTTGATGACTACATGATG 1320  
QY 1321 GGGAGTGTGATCAAAATGCCAAAGTAGCTGATGTAGGAGTGTCTAAATGAGTAGATG 1380  
DB 1321 GGGAGTGTGATCAAAATGCCAAAGTAGCTGATGTAGGAGTGTCTAAATGAGTAGATG 1380  
QY 1381 AATATTCGTGTTCTTCAGAGAAATAGACTTACTGGCCAGTATCTCATGAGGCTTTAA 1440  
DB 1381 AATATTCGTGTTCTTCAGAGAAATAGACTTACTGGCCAGTATCTCATGAGGCTTTAA 1440  
QY 1441 TAGTAAATGAGAGGTTCTACCTCCAAATCAGTAGAGATATATTTGAAGACAAATAT 1500  
DB 1441 TAGTAAATGAGAGGTTCTACCTCCAAATCAGTAGAGATATATTTGAAGACAAATAT 1500  
QY 1501 TTGGGAAACCTATCGGAAAGGCAAGGCTCCCACTTAAGCCATGATAGTAAATATC 1560  
DB 1501 TTGGGAAACCTATCGGAAAGGCAAGGCTCCCACTTAAGCCATGATAGTAAATATC 1560  
QY 1561 TAATTAATGAGAGATTTGTTACTGAGCCACAGATATATACAGAGGCTCCCTCACAATA 1620  
DB 1561 TAATTAATGAGAGATTTGTTACTGAGCCACAGATATATACAGAGGCTCCCTCACAATA 1620  
QY 1621 AATTTAAAGGCTAAAAGAGACCTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTTAAAGGCTAAAAGAGACCTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGAGTTCAAAAGACCTCTGAATATGATTAATCAAGGGAACCTAACCAAGGAGC 1740  
DB 1681 CAGATTTGGAGTTCAAAAGACCTCTGAATATGATTAATCAAGGGAACCTAACCAAGGAGC 1740  
QY 1741 AGATGCTCAAGTATGATTAATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
DB 1741 AGATGCTCAAGTATGATTAATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
QY 1801 CTATTCGAGATGAGAAAAATCTTACCCATAGATATGATCTCGAAAAAGATCTGCTTTCA 1860  
DB 1801 CTATTCGAGATGAGAAAAATCTTACCCATAGATATGATCTCGAAAAAGATCTGCTTTCA 1860  
QY 1861 AAAGGAAAGCTGAACCTATTAAGAGAGAGTATTAAGCAATATGGAATTAATATTC 1920  
DB 1861 AAAGGAAAGCTGAACCTATTAAGAGAGAGTATTAAGCAATATGGAATTAATATTC 1920  
QY 1921 ACAATTCAAAAGACCTTAAAGAGATAGGCTGAGAGAGAGTCTTCTACAGAGCATATTC 1980  
DB 1921 ACAATTCAAAAGACCTTAAAGAGATAGGCTGAGAGAGAGTCTTCTACAGAGCATATTC 1980  
QY 1981 ATGCGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
DB 1981 ATGCGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
QY 2041 TTGATTAATGTTGTTAGAGAGTGAAGAGATTAAGAAAAAGTAAACCAATATGCAATCA 2100  
DB 2041 TTGATTAATGTTGTTAGAGAGTGAAGAGATTAAGAAAAAGTAAACCAATATGCAATCA 2100  
QY 2101 GGCACAGACAGAAACCTTCAACTCATGAGAGTAAAGAACTGCAACTGAGAGCCAAAGAGA 2160  
DB 2101 GGCACAGACAGAAACCTTCAACTCATGAGAGTAAAGAACTGCAACTGAGAGCCAAAGAGA 2160  
QY 2161 GTAAACAGGCAATTAAGACAGACAGTAAAGAGACATGACAGGATCTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGGCAATTAAGACAGACAGTAAAGAGACATGACAGGATCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGACCTGTTCTTCTTACTAAGTGTCAATTAACAGGATTAAGAAAT 2280  
DB 2221 AGTTAAACAAATGACCTGTTCTTCTTACTAAGTGTCAATTAACAGGATTAAGAAAT 2280  
QY 2281 TTGTCATCTAGGCTTCCAG 2340  
DB 2281 TTGTCATCTAGGCTTCCAG 2340

QY 2341 CTAATAATGCTGAAG 2400  
DB 2341 CTAATAATGCTGAAG 2400  
QY 2401 AAAGATCTGAG 2460  
DB 2401 AAAGATCTGAG 2460  
QY 2461 AAAGATCTGAG 2520  
DB 2461 AAAGATCTGAG 2520  
QY 2521 GTGTGAGTCAAGTGTGAG 2580  
DB 2521 GTGTGAGTCAAGTGTGAG 2580  
QY 2581 ATATTAATGAG 2640  
DB 2581 ATATTAATGAG 2640  
QY 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2700  
DB 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2700  
QY 2701 TCAAGGTTTCAAGAGGCGGACATTTGCTGTTTCAATCCAGAGAAATGCAAGAGAG 2760  
DB 2701 TCAAGGTTTCAAGAGGCGGACATTTGCTGTTTCAATCCAGAGAAAGTGAAGAGAG 2760  
QY 2761 AATGTCACATTTCTGCGCCACATCTGCTGCTTAAAGAAACCAAGTCCAAAGTCACT 2820  
DB 2761 AATGTCACATTTCTGCGCCACATCTGCTGCTTAAAGAAACCAAGTCCAAAGTCACT 2820  
QY 2821 TTGAATGTGAACAAAG 2880  
DB 2821 TTGAATGTGAACAAAG 2880  
QY 2881 AGACAGTATATATCAGTGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940  
DB 2881 AGACAGTATATATCAGTGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940  
QY 2941 ATGCAAAATGATATCAAG 3000  
DB 2941 ATGCAAAATGATATCAAG 3000  
QY 3001 ACAGAACTGAGCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3060  
DB 3001 ACAGAACTGAGCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAACCTAATGTAAGAAAAATCTGCTAGAG 3120  
DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAACCTAATGTAAGAAAAATCTGCTAGAG 3120  
QY 3121 AAAAATTTGAGGAACATTAATGATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180  
DB 3121 AAAAATTTGAGGAACATTAATGATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180  
QY 3181 GTACAGTGAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3240  
DB 3181 GTACAGTGAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3240  
QY 3241 CAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3300  
DB 3241 CAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3300  
QY 3301 TAGGTTCCAGTGAAGAAACATTAAGCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3360  
DB 3301 TAGGTTCCAGTGAAGAAACATTAAGCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3360  
QY 3361 ATGCTATGCTTGAATTAAGAGGTTTGAACCTGAGGCTTAATTAAGCAAGTCTCTGGAAG 3420  
DB 3361 ATGCTATGCTTGAATTAAGAGGTTTGAACCTGAGGCTTAATTAAGCAAGTCTCTGGAAG 3420  
QY 3421 GTAAATTTGAAGCATCTGAAATTAAGCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGA 3480

```
Db 3421 GTATTTGTAAGCATCCGTAATAAAGCAAGATATGAAAGTAAGTATGATGATGTTA 3480
Oy 3481 ATACAGATTTCTCTCCATATCTGATTCAGATTAATTAAGAACAGCCTTGGGAAGTACTC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTCAGATTAATTAAGAACAGCCTTGGGAAGTACTC 3540
Oy 3541 ATGCATCTCAGGTTTGTTCGAGACACCTGATGACCTGTTGATGATGATGTTGTAATTAAGG 3600
Db 3541 ATGCATCTCAGGTTTGTTCGAGACACCTGATGACCTGTTGATGATGATGTTGTAATTAAGG 3600
Oy 3601 AAGATCTAGTTTGTGTAATAATGACATTAAGAAAGTTGCTGTTTGAACAAAGCG 3660
Db 3601 AAGATCTAGTTTGTGTAATAATGACATTAAGAAAGTTGCTGTTTGAACAAAGCG 3660
Oy 3661 TCCAGAAAGAGAGCCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG 3720
Oy 3721 GTTACCGAAGAGGAGCCCAAGAAATTAAGTCTCTGAGAGAGACTTATCTAGTGAGATG 3780
Db 3721 GTTACCGAAGAGGAGCCCAAGAAATTAAGTCTCTGAGAGAGACTTATCTAGTGAGATG 3780
Oy 3781 AAGAGCTTCCCTGCTCCACACTTGTATTGTTAAAGTAAGCAATATACCTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTCCACACTTGTATTGTTAAAGTAAGCAATATACCTCTCAGT 3840
Oy 3841 CTACTAGGCAATAGCACCAGTGTCTACCGAGTGTCTGTAGAACACAGAGAGAGATTTAT 3900
Db 3841 CTACTAGGCAATAGCACCAGTGTCTACCGAGTGTCTGTAGAACACAGAGAGATTTAT 3900
Oy 3901 TATCATTTGAAGATAGCTTAAATGATCAGTACAGTAATTTGGCAAGGACATCTC 3960
Db 3901 TATCATTTGAAGATAGCTTAAATGATCAGTACAGTAATTTGGCAAGGACATCTC 3960
Oy 3961 AGGACATCACTTGTAGTGAAGAAACAAATGTTCTGCTAGCTTCTTCTCAGAGTGA 4020
Db 3961 AGGACATCACTTGTAGTGAAGAAACAAATGTTCTGCTAGCTTCTTCTCAGAGTGA 4020
Oy 4021 GTGAAATTTGGAAGACTTGACGCAAAATCAAAACCCAGAGATCTTCTGATTTGGTCTT 4080
Db 4021 GTGAAATTTGGAAGACTTGACGCAAAATCAAAACCCAGAGATCTTCTGATTTGGTCTT 4080
Oy 4081 CCAAAACAATGAGGCACTGATGTAAGCCAGGAGTTGCTGAGTGAACAAGAAATTGG 4140
Db 4081 CCAAAACAATGAGGCACTGATGTAAGCCAGGAGTTGCTGAGTGAACAAGAAATTGG 4140
Oy 4141 TTTGAGATGATGAAGAAAGAGAAAGGCTTGGAAAGAAATTAATCAAGAAAGCAAGCA 4200
Db 4141 TTTGAGATGATGAAGAAAGAGAAAGGCTTGGAAAGAAATTAATCAAGAAAGCAAGCA 4200
Oy 4201 TGGATTCAAAACCTTAGGGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAG 4260
Db 4201 TGGATTCAAAACCTTAGGGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAG 4260
Oy 4261 ACTGCTCAGGGGCTATCCTCTCAGAGTGAATTTTAACCATCTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGGGCTATCCTCTCAGAGTGAATTTTAACCATCTCAGCAGAGGATACCATGC 4320
Oy 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAATAGAACTGTGTAGAACAGC 4380
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAATAGAACTGTGTAGAACAGC 4380
Oy 4381 ATGGAGGCCAGCCTTCTAACAGTACCCCTTCATCATTAAGTGAAGTCTTCTGAGGCTTGG 4440
Db 4381 ATGGAGGCCAGCCTTCTAACAGTACCCCTTCATCATTAAGTGAAGTCTTCTGAGGCTTGG 4440
Oy 4441 ACCTGGAATCCAGAAACAGACATCAGAAAAAGAGATTAATTAATTAATTAATTAATTAATTA 4500
Db 4441 ACCTGGAATCCAGAAACAGACATCAGAAAAAGAGATTAATTAATTAATTAATTAATTAATTA 4500
Oy 4501 GTGAATACCTATTAAGCAGAAATCAGAAAGGCTTCTGCTGACAAAGTGGAGGTCTG 4560
Db 4501 GTGAATACCTATTAAGCAGAAATCAGAAAGGCTTCTGCTGACAAAGTGGAGGTCTG 4560
```

---

```
Db 4501 GTGAATACCTATTAAGCAGAAATCAGAAAGGCTTCTGCTGACAAAGTGGAGGTCTG 4560
Oy 4561 CAGATAGCTTACACAGTAAATAAAGAACACAGAGTGAAGAGTATCCCTTCTTAAT 4620
Db 4561 CAGATAGCTTACACAGTAAATAAAGAACACAGAGTGAAGAGTATCCCTTCTTAAT 4620
Oy 4621 GCCCATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680
Db 4621 GCCCATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680
Oy 4681 ACTACCATCTCAAGAGAGAGTCTTAAGGTTGTTGATGATGATGATGATGATGATGATGATG 4740
Db 4681 ACTACCATCTCAAGAGAGAGTCTTAAGGTTGTTGATGATGATGATGATGATGATGATGATG 4740
Oy 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGGCCAAAGCAAGATCTAGAGGGA 4800
Db 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGGCCAAAGCAAGATCTAGAGGGA 4800
Oy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGATGATGATGATGATGATGATGATGATG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGATGATGATGATGATGATGATGATGATG 4860
Oy 4861 AAGACAGAGCCCAAGTCAAGTCTGTTGGAACATACCATCTCAACCTGCAATGA 4920
Db 4861 AAGACAGAGCCCAAGTCAAGTCTGTTGGAACATACCATCTCAACCTGCAATGA 4920
Oy 4921 AAGTTCCCAATTAAGATTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980
Db 4921 AAGTTCCCAATTAAGATTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980
Oy 4981 ATACTGCTGGGATTAATGCAATGGAAGAAAGTGTGACAGAGGAAGCCAGATTTGACAG 5040
Db 4981 ATACTGCTGGGATTAATGCAATGGAAGAAAGTGTGACAGAGGAAGCCAGATTTGACAG 5040
Oy 5041 CTTCACAGAAAGGCTCAACAAAGAAATGTCATGGTGGTGTGCTGAGCCAGCCAGAG 5100
Db 5041 CTTCACAGAAAGGCTCAACAAAGAAATGTCATGGTGGTGTGCTGAGCCAGCCAGAG 5100
Oy 5101 AATTTATGCTGTGTACAGATTTGCCAGAAACACACATCACTTAATTAATTAATTAATTA 5160
Db 5101 AATTTATGCTGTGTACAGATTTGCCAGAAACACACATCACTTAATTAATTAATTAATTA 5160
Oy 5161 CTGAAGAGTACTCATGTTGTTATGAAAAACAGATCTTAAGTTGTGTGAACGAGAC 5220
Db 5161 CTGAAGAGTACTCATGTTGTTATGAAAAACAGATCTTAAGTTGTGTGAACGAGAC 5220
Oy 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTGAATTTCTGCTGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTGAATTTCTGCTGGTGACCC 5280
Oy 5281 AGTCTATTTAAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGAG 5340
Db 5281 AGTCTATTTAAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGAG 5340
Oy 5341 TCAATGGAAGAAACCAAGGTCGCAAGGCAAGCAAGAAATCCAGAGCAACAAAGATCT 5400
Db 5341 TCAATGGAAGAAACCAAGGTCGCAAGGCAAGCAAGAAATCCAGAGCAACAAAGATCT 5400
Oy 5401 TCAAGGGGCTAGAAATCTGTGCTATGAGGCGCTTCAACCAATGCCCAGATCAACTGG 5460
Db 5401 TCAAGGGGCTAGAAATCTGTGCTATGAGGCGCTTCAACCAATGCCCAGATCAACTGG 5460
Oy 5461 AATGATGTTGACAGCTGTGTGCTCTGTGTGTAAGAGGCTTTCATCATTTACACCTTG 5520
Db 5461 AATGATGTTGACAGCTGTGTGCTCTGTGTGTAAGAGGCTTTCATCATTTACACCTTG 5520
Oy 5521 GCACAGTGTCCACCAATTTGTTGTGTGACAGCAGATCTCTGACAGAGCAATGCT 5580
Db 5521 GCACAGTGTCCACCAATTTGTTGTGTGACAGCAGATCTCTGACAGAGCAATGCT 5580
Oy 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGTGTTGGACA 5640
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGTGTTGGACA 5640
```

QY 5641 GGTAGCACTTACCACTGCGAGAGCTGGACACCT-ACCTGATACCCAGATCCCCAC 5699  
|||||  
DB 5641 GGTAGCACTTACCACTGCGAGAGCTGGACACCTAACCCTGATACCCAGATCCCCAC 5700  
QY 5700 AGCCACTACTGA 5711  
|||||  
DB 5701 AGCCACTACTGA 5712  
|||||  
RESULT 15  
LOCUS I40797 5710 bp DNA PAT 01-MAY-1997  
DEFINITION Sequence 6 from patent US 5622829.  
ACCESSION I40797  
NID 92082277  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5710)  
AUTHORS King, M., Friedman, L., Ostermeyer, B., Rowell, S., Lynch, E., Szabo, C.  
and Lee, M.  
TITLE Genetic markers for breast, ovarian, and prostatic cancer  
JOURNAL Patent: US 5622829-A 6 22-Apr-1997;  
FEATURES  
source 1..5710  
1..5710  
/organism="Unknown"  
BASE COUNT 1955 a 1099 c 1274 g 1382 t  
ORIGIN

Query Match 99.8%; Score 5697.4; DB 6; Length 5710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5709; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AGCTGCTGAGACTTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAATACTGGCC 60  
|||||  
DB 1 AGCTGCTGAGACTTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAATACTGGCC 60  
QY 61 CCTGGCTGAGAGGCGCTTACCCCTGCTGGTGAAGTTGATTTGAAGCAAGAA 120  
|||||  
DB 61 CCTGGCTGAGAGGCGCTTACCCCTGCTGGTGAAGTTGATTTGAAGCAAGAA 120  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAAGTACAAATGTATTATGCTATGCA 180  
|||||  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAAGTACAAATGTATTATGCTATGCA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCACAAGTGTGACC 240  
|||||  
DB 181 TCTTAGAGTGTCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCACAAGTGTGACC 240  
QY 241 ACATATTTTGAATTTTGCATGCTGAACCTTCAACAGAAAGGCGCTTCACAGT 300  
|||||  
DB 241 ACATATTTTGAATTTTGCATGCTGAACCTTCAACAGAAAGGCGCTTCACAGT 300  
QY 301 GTCCTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAAAGTACGAGATTAGTC 360  
|||||  
DB 301 GTCCTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAAAGTACGAGATTAGTC 360  
QY 361 AACTTGTGAAGAGCTATTTGAAGAAATCATTTGTCTTTGAGCTTGACAGGTTTGAAT 420  
|||||  
DB 361 AACTTGTGAAGAGCTATTTGAAGAAATCATTTGTCTTTGAGCTTGACAGGTTTGAAT 420  
QY 421 ATGCAAAAGAGCTATTTTGAAGAAAGAAATTAATCTCTGGAACATCTTAAAGATG 480  
|||||  
DB 421 ATGCAAAAGAGCTATTTTGAAGAAAGAAATTAATCTCTGGAACATCTTAAAGATG 480  
QY 481 AACTTCTATCATCAAAAGTATGGGTACAGAAACCGTGCAAAAGACTTCTACAGAGTG 540  
|||||  
DB 481 AACTTCTATCATCAAAAGTATGGGTACAGAAACCGTGCAAAAGACTTCTACAGAGTG 540  
QY 541 AACCCGAATATCTTCTTGGCAGAGAAACAGTCTCAGTGTCAACTCTTAACCTTGGAA 600  
|||||

DB 541 AACCCGAATATCTTCTTGGCAGAGAAACAGTCTCAGTGTCAACTCTTAACTTTGGAA 600  
|||||  
QY 601 CTGTGAGAACTGTGAGAGCAAAAGCAGCGGATACAACTCAAAAGAGTGTCTACATG 660  
|||||  
DB 601 CTGTGAGAACTGTGAGAGCAAAAGCAGCGGATACAACTCAAAAGAGTGTCTACATG 660  
QY 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATTAAGCAACTTATTCAGTGGGAG 720  
|||||  
DB 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATTAAGCAACTTATTCAGTGGGAG 720  
QY 721 ATCAAGAAATGTTACAAATCAACCCCTCAAGGAAACAGGATGAATTCGATTCG 780  
|||||  
DB 721 ATCAAGAAATGTTACAAATCAACCCCTCAAGGAAACAGGATGAATTCGATTCG 780  
QY 781 CAAAAAGGCTGCTTGTGAAATTTCTGAGAGCGGATGAACAATCTGAAATCATCAAC 840  
|||||  
DB 781 CAAAAAGGCTGCTTGTGAAATTTCTGAGAGCGGATGAACAATCTGAAATCATCAAC 840  
QY 841 CCAGTAATATGATTTGAACACCACTGAGAGCGGTGACGCTGAGAGGATCCAGAAAGT 900  
|||||  
DB 841 CCAGTAATATGATTTGAACACCACTGAGAGCGGTGACGCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGATGCTGCTGTTCAACTGCAATGAGGCAATGGCAATGTCATGCA 960  
|||||  
DB 901 ATCAGGATGCTGCTGTTCAACTGCAATGAGGCAATGTCATGCA 960  
QY 961 GCTCATTTACAGCATGAGAACAGCAGTTTATCTCACTAATAACAGAAATGATGAAA 1020  
|||||  
DB 961 GCTCATTTACAGCATGAGAACAGCAGTTTATCTCACTAATAACAGAAATGATGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGCTTACCAAGAGCCAACTTAACAGAT 1080  
|||||  
DB 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGCTTACCAAGAGCCAACTTAACAGAT 1080  
QY 1081 GGGCTGGAATGAGAAACATGTAATGAGGCGGACCTCCGACAGAAAGAAAGTGA 1140  
|||||  
DB 1081 GGGCTGGAATGAGAAACATGTAATGAGGCGGACCTCCGACAGAAAGAAAGTGA 1140  
QY 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGAAATGAAATGAGAGAACTGCCATGCT 1200  
|||||  
DB 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGAAATGAAATGAGAGAACTGCCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATGATGATGCTTGGATTAACCTAATATGACAGATTCAGA 1260  
|||||  
DB 1201 CAGAGAACTCTAGAGATGATGATGCTTGGATTAACCTAATATGACAGATTCAGA 1260  
QY 1260 AAGTTAATAGTGTTCACAAAGATGATGAAGTGTGATGATGATGATGATGATG 1320  
|||||  
DB 1260 AAGTTAATAGTGTTCACAAAGATGATGAAGTGTGATGATGATGATGATGATG 1320  
QY 1321 GGGAGCTGAATCAATGCAAGTATGATGATGATGATGATGATGATGATGATGATG 1380  
|||||  
DB 1321 GGGAGCTGAATCAATGCAAGTATGATGATGATGATGATGATGATGATGATGATG 1380  
QY 1381 AATATTCTGCTTCTGAGAAATGACTTACTGCGCAGTATCTCTCATGAGGCTTTAA 1440  
|||||  
DB 1381 AATATTCTGCTTCTGAGAAATGACTTACTGCGCAGTATCTCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAGTGAAGAGTCACTCCAAATCACTGAGAGTATATGTAAGCAAAATAT 1500  
|||||  
DB 1441 TATGTAAGTGAAGAGTCACTCCAAATCACTGAGAGTATATGTAAGCAAAATAT 1500  
QY 1501 TTGGGAAAACCTATGGAAGAGCAAGCTCCCAACTTAAGCCATGTAAGTGAATATC 1560  
|||||  
DB 1501 TTGGGAAAACCTATGGAAGAGCAAGCTCCCAACTTAAGCCATGTAAGTGAATATC 1560  
QY 1561 TAATTAAGAGATTTGTTACTGAGCCAGATTAATACAGAGGCTCCCTACAAATA 1620  
|||||  
DB 1561 TAATTAAGAGATTTGTTACTGAGCCAGATTAATACAGAGGCTCCCTACAAATA 1620  
QY 1621 AATTAAGGCTAAAGGAACTACATCGGCTCATCTGAGGATTTATCAAGAAAG 1680  
|||||

Db 1620 AATTAAAGCGTAAAGAGACCTACATCAGGCCCTTCATCTGAGATTTTATTCAGAAAG 1679  
QY 1681 CAGATTTGGCAGTTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATAACCAAGGAGAC 1740  
Db 1680 CAGATTTGGCAGTTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATAACCAAGGAGAC 1739  
QY 1741 AGAATGGTCAGATGATGAAATATTTACTAATAGTGTCTAGAGAAATTAACAAAGGTGATT 1800  
Db 1740 AGAATGGTCAGATGATGAAATATTTACTAATAGTGTCTAGAGAAATTAACAAAGGTGATT 1799  
QY 1801 CTATTCAGATGAGAAATATCTTAACCCATAGTAATCACTCGAAAAAGAAATGCGTTTCA 1860  
Db 1800 CTATTCAGATGAGAAATATCTTAACCCATAGTAATCACTCGAAAAAGAAATGCGTTTCA 1859  
QY 1861 AAACGAAAGCTGAACCTTATAGCAGCAGTATTAAGCAATATGGAAGTCTGAATTAATATCC 1920  
Db 1860 AAACGAAAGCTGAACCTTATAGCAGCAGTATTAAGCAATATGGAAGTCTGAATTAATATCC 1919  
QY 1921 ACAATTTCAAAAGCAGCTTAAAGAAATAGGCTGAGAGAGAAAGCTTCTACAGGCAATATTC 1980  
Db 1920 ACAATTTCAAAAGCAGCTTAAAGAAATAGGCTGAGAGAGAAAGCTTCTACAGGCAATATTC 1979  
QY 1981 ATGCGCTTGAAGTACTAGTACTAGTAAATCTAAGCCCACTAATGTGACTGAAATGCAAA 2040  
Db 1980 ATGCGCTTGAAGTACTAGTACTAGTAAATCTAAGCCCACTAATGTGACTGAAATGCAAA 2039  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2100  
Db 2040 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2099  
QY 2101 GGCACAGAGAAACCTTAACATCATGAGAAAGTAAAGAAACCTCAACTGAGAGCAAGAA 2160  
Db 2100 GGCACAGAGAAACCTTAACATCATGAGAAAGTAAAGAAACCTCAACTGAGAGCAAGAA 2159  
QY 2161 GTAACAGGCCAAATGAGACAGCAATTAAGAAAGACATGACAGCATCTTCCAGAGCTGA 2220  
Db 2160 GTAACAGGCCAAATGAGACAGCAATTAAGAAAGACATGACAGCATCTTCCAGAGCTGA 2219  
QY 2221 AGTTAACAAATGACACCTGCTTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2280  
Db 2220 AGTTAACAAATGACACCTGCTTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2279  
QY 2281 TTGTCATTCCTAGCAGCTTCCAGAGAGAAAGAAAGAGAAATTAAGAAAGTAAAGCT 2340  
Db 2280 TTGTCATTCCTAGCAGCTTCCAGAGAGAAAGAAAGAGAAATTAAGAAAGTAAAGCT 2339  
QY 2341 CTAATTAATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTCCAACTG 2400  
Db 2340 CTAATTAATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTCCAACTG 2399  
QY 2401 AAAGATCTGTGAAGAGTGAAGATTTTCAATGTTGTAAGTGAAGAAAGGTTTCCAACTG 2460  
Db 2400 AAAGATCTGTGAAGAGTGAAGATTTTCAATGTTGTAAGTGAAGAAAGGTTTCCAACTG 2459  
QY 2461 AAAGTATCTGTTACTGGAAGTGAAGTGAAGTGAAGGAGGAAAGAAACAGAACCAATTAAT 2520  
Db 2460 AAAGTATCTGTTACTGGAAGTGAAGTGAAGTGAAGGAGGAAAGAAACAGAACCAATTAAT 2519  
QY 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGAGCAATATTCATGTTGTTCCAAAG 2580  
Db 2520 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGAGCAATATTCATGTTGTTCCAAAG 2579  
QY 2581 ATATATGAAATGACACAGAGGCTTTAAGTATCCATTGGGAGATGAAGTTAAACACAGTC 2640  
Db 2580 ATATATGAAATGACACAGAGGCTTTAAGTATCCATTGGGAGATGAAGTTAAACACAGTC 2639  
QY 2641 GGGAAAGACAGATGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700  
Db 2640 GGGAAAGACAGATGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2699  
QY 2701 TCAAGGTTTCAAGAGCGCAGTCAATTTGCTGTGTTTCAATTCAGGAATGAGAGAGG 2760  
Db 2700 TCAAGGTTTCAAGAGCGCAGTCAATTTGCTGTGTTTCAATTCAGGAATGAGAGAGG 2759

QY 2761 AATGTGCAACATTTCTCTGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2760 AATGTGCAACATTTCTCTGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2819  
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGATGATCTTAATATCAAGCTGTAC 2880  
Db 2820 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGATGATCTTAATATCAAGCTGTAC 2879  
QY 2881 AGACAGTAAATATCACTCAGGCTTCTGTGTGGTGCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2880 AGACAGTAAATATCACTCAGGCTTCTGTGTGGTGCAGAAAGATTAAGCCAGTTGATA 2939  
QY 2941 ATGCCAAATGTATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Db 2940 ATGCCAAATGTATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 2999  
QY 3001 ACGAAGCTGAGCTCATCTCTCCAAATTAACATGAGACCTTTTCAAAACCCATATGCTATAC 3060  
Db 3000 ACGAAGCTGAGCTCATCTCTCCAAATTAACATGAGACCTTTTCAAAACCCATATGCTATAC 3059  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAATCTGCTAGAGG 3120  
Db 3060 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAATCTGCTAGAGG 3119  
QY 3121 AAACTTTGAGGACATTCATGTCACCTGAAGAGAAATGGCAATGAGAACATTTCCAA 3180  
Db 3120 AAACTTTGAGGACATTCATGTCACCTGAAGAGAAATGGCAATGAGAACATTTCCAA 3179  
QY 3181 GTACAGTGAAGACATTTGCGGTATTAACATTAAGAAATGTTTAAAGAAAGCCAGCT 3240  
Db 3180 GTACAGTGAAGACATTTGCGGTATTAACATTAAGAAATGTTTAAAGAAAGCCAGCT 3239  
QY 3241 CAAGCAATATTAATGAAGTGAAGTTCAGTACTAATGAAGTGGGCTCCAGATTAATGAAG 3300  
Db 3240 CAAGCAATATTAATGAAGTGAAGTTCAGTACTAATGAAGTGGGCTCCAGATTAATGAAG 3299  
QY 3301 TAGGTTCCAGTGAATGAAGAAATTCAGCAGACATGAGTGAAGAAAGAGGCGCAAAATTTGA 3360  
Db 3300 TAGGTTCCAGTGAATGAAGAAATTCAGCAGACATGAGTGAAGAAAGAGGCGCAAAATTTGA 3359  
QY 3361 ATGCTATGCTTAGATTTAGGGGTTTGAACCTGAGGCTAATTAACAAAGTCTCTGAGAA 3420  
Db 3360 ATGCTATGCTTAGATTTAGGGGTTTGAACCTGAGGCTAATTAACAAAGTCTCTGAGAA 3419  
QY 3421 GTAATTTGAACATCTCTGAAGTAAAGAAAGCAAGAAATGAAGAAAGTGAAGTGAAGTGAAG 3480  
Db 3420 GTAATTTGAACATCTCTGAAGTAAAGAAAGCAAGAAATGAAGAAAGTGAAGTGAAGTGAAG 3479  
QY 3481 ATACAGATTTTCTCTCAGATATGATTTTCAATTAAGTGAAGAAAGCTTAAGGAAATGATC 3540  
Db 3480 ATACAGATTTTCTCTCAGATATGATTTTCAATTAAGTGAAGAAAGCTTAAGGAAATGATC 3539  
QY 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGATGATGATGATG 3600  
Db 3540 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGATGATGATGATG 3599  
QY 3601 AAGATCTAGTTTGTCTGAAGAAATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3660  
Db 3600 AAGATCTAGTTTGTCTGAAGAAATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3659  
QY 3661 TCCAGAAAGAGAGCTTGAAGAGAGTCTAGGCTTTTACCCATACATTTGGCTCAGG 3720  
Db 3660 TCCAGAAAGAGAGCTTGAAGAGAGTCTAGGCTTTTACCCATACATTTGGCTCAGG 3719  
QY 3721 GTTACCGAAGAGGCGCAAGAAATTAAGATTCCTAGAGAGAAAGTCTTCAAGAGAGATG 3780  
Db 3720 GTTACCGAAGAGGCGCAAGAAATTAAGATTCCTAGAGAGAAAGTCTTCAAGAGAGATG 3779  
QY 3781 AAGAGCTTCCCTGCTTCCACACATTTGTTATTTGTTAAGTAAACAAATATCTCTCAGT 3840  
Db 3780 AAGAGCTTCCCTGCTTCCACACATTTGTTATTTGTTAAGTAAACAAATATCTCTCAGT 3839



OY	384.1	CTCTAGGCAATAGCACCCTTGTCACCGAGGTCGTCTTAAGAAACAACAGAGAAATTTAT	3900
Db	384.0	CTACTAGGCAATAGCACCCTTGTCACCGAGGTCGTCTTAAGAAACAACAGAGGAATTTAT	3899
OY	390.1	TATCATTTGAAGAATAGCTTTAAATGACTGTCAGTAAACAGGATTAATATGGCAAAAGCATCTC	3960
Db	390.0	TATCATTTGAAGAATAGCTTTAAATGACTGTCAGTAAACAGGATTAATATGGCAAAAGCATCTC	3959
OY	396.1	AGGAACATCACCTTATAGTAGGAAACAAAATGTTCTGCTAGTCTGTTTCTTCACAGTGCA	4020
Db	396.0	AGGAACATCACCTTATAGTAGGAAACAAAATGTTCTGCTAGTCTGTTTCTTCACAGTGCA	4019
OY	402.1	GTCGAATTTGGAAGACTTTCACGTGCAAAATTAACAACCCAGGATCCCTTCTTGTGATGGTCTT	4080
Db	402.0	GTCGAATTTGGAAGACTTTCACGTGCAAAATTAACAACCCAGGATCCCTTCTTGTGATGGTCTT	4079
OY	408.1	CCAACAACAAATAGAGCATCACTCTGAAGAGCAGAGGATTTGCTGTAGTGACAAAGAAATGG	4140
Db	408.0	CCAACAACAAATAGAGCATCACTCTGAAGAGCAGAGGATTTGCTGTAGTGACAAAGAAATGG	4139
OY	414.1	TTTTCAGATGATGAAGAAAGGAAGCGGGCTTGGAGAAAATTAATCAAGAGACAAACGA	4200
Db	414.0	TTTTCAGATGATGAAGAAAGGAAGCGGGCTTGGAGAAAATTAATCAAGAGACAAACGA	4199
OY	420.1	TGGAATTTAAACTTAAGTGAAGAGCACTCTGGGTGTGAAGTAAACAACGCTCTCTGAG	4260
Db	420.0	TGGAATTTAAACTTAAGTGAAGAGCACTCTGGGTGTGAAGTAAACAACGCTCTCTGAG	4259
OY	426.1	ACTGCTCAGAGGCTATCCTCTCAGAGTGAACATTTTAAACCTCAGAGAGGGGATACATGC	4320
Db	426.0	ACTGCTCAGAGGCTATCCTCTCAGAGTGAACATTTTAAACCTCAGAGAGGGGATACATGC	4319
OY	432.1	AACATTAACCTGATTAAGCTTCACAGAGGAAATGGCTGAATAGAACCTGTGTAGAACAGC	4380
Db	432.0	AACATTAACCTGATTAAGCTTCACAGAGGAAATGGCTGAATAGAACCTGTGTAGAACAGC	4379
OY	438.1	ATGGGAGCCAGCCTTCTTAACAGGTACCCTTCATATAAGTACCTTCTGCCCTTGAGG	4440
Db	438.0	ATGGGAGCCAGCCTTCTTAACAGGTACCCTTCATATAAGTACCTTCTGCCCTTGAGG	4439
OY	444.1	ACCTGCAAAATTCAGAAACAAGACATCAAGAAAAGCAGTATTAATCTTCACAGAAAAGTA	4500
Db	444.0	ACCTGCAAAATTCAGAAACAAGACATCAAGAAAAGCAGTATTAATCTTCACAGAAAAGTA	4499
OY	450.1	GTCGAATACCCTTAAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTGAGGTCTG	4560
Db	450.0	GTCGAATACCCTTAAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTGAGGTCTG	4559
OY	456.1	CAGATAGTTTCTACCATGTTAAAAATAAAGAACACAGAGTGGAAAGTCAATCCCTCTTAAT	4620
Db	456.0	CAGATAGTTTCTACCATGTTAAAAATAAAGAACACAGAGTGGAAAGTCAATCCCTCTTAAT	4619
OY	462.1	GCCCATATTAGATGATAGGTGGTACATCACAAGTTGCTGCTGGAGCTTCAGAAATAGAA	4680
Db	462.0	GCCCATATTAGATGATAGGTGGTACATCACAAGTTGCTGCTGGAGCTTCAGAAATAGAA	4679
OY	468.1	ACTACCCATCTCAAGAGGAGACTCATTAAGGTTGTTGATGTGAGAGCAACAGCTGAGAG	4740
Db	468.0	ACTACCCATCTCAAGAGGAGACTCATTAAGGTTGTTGATGTGAGAGCAACAGCTGAGAG	4739
OY	474.1	AGTGTGGGCCACACAGATTTGACGGAACATCTTACTTCCCAAGCAAGATCTAGAGGAA	4800
Db	474.0	AGTGTGGGCCACACAGATTTGACGGAACATCTTACTTCCCAAGCAAGATCTAGAGGAA	4799
OY	480.1	CCCCCTTAACCTGGAGATCTGGAAATAGGCTCTTCTCTGATGACCTTAATCTATCTCTTG	4860
Db	480.0	CCCCCTTAACCTGGAGATCTGGAAATAGGCTCTTCTCTGATGACCTTAATCTATCTCTTG	4859
OY	486.1	AAGACAGAGCCCGAGAGTCAAGTCTGTGTGGCAACAATACATCTTCAACCTGTGATGTA	4920
Db	486.0	AAGACAGAGCCCGAGAGTCAAGTCTGTGTGGCAACAATACATCTTCAACCTGTGATGTA	4919
OY	492.1	AAGTTCGCCCAATTGAAGTTCAGAAATCTGCCAGAGTCCAGCTGCTGCTATACACTAG	4980

Db	4920	AAAGTCCCAATGAAAGGTGCAGAAATCTGCCAGAGTCACAGCTCTGCTCATCTACTG	4979
Qy	4981	ATATCTGCTGGGTATATATGCAATGAGAAAGTGTGACGAGGAGAGACAGAAATTTGACG	5040
Db	4980	ATATCTGCTGGGTATATATGCAATGAGAAAGTGTGACGAGGAGAGACAGAAATTTGACG	5039
Qy	5041	CTTCACACGAAAGGGTCCACAAAAGATTCATGGTGTCTGTGGCTGACCCGACAG	5100
Db	5040	CTTCACACGAAAGGGTCCACAAAAGATTCATGGTGTCTGTGGCTGACCCGACAG	5099
Qy	5101	AATTTATGTCGCTGTACAACTTTGCCAGAAAACACATCTACTTAATCTAATTA	5160
Db	5100	AATTTATGTCGCTGTACAACTTTGCCAGAAAACACACATCTTAATCTAATTA	5159
Qy	5161	CTGAGAGACACTCATGTGTATGAAAACAGATGCTAGTTGTGTGTCAGACGAC	5220
Db	5160	CTGAGAGACACTCATGTGTATGAAAACAGATGCTAGTTGTGTGTCAGACGAC	5219
Qy	5221	TGAAATATTTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACC	5280
Db	5220	TGAATATTTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACC	5279
Qy	5281	AGCTATTTAAAGAAAGAAAAATCTCAATGACATGATTTTAAATCTAGAGAGATGTGG	5340
Db	5280	AGCTATTTAAAGAAAGAAAAATCTCAATGACATGATTTTAAATCTAGAGAGATGTGG	5339
Qy	5341	TCATATGGAAGAAACACCAAGGTCTCAAACGAGCAAGAAATCCCAAGACAGAAAGATCT	5400
Db	5340	TCAATATGGAAGAAACACCAAGGTCTCAAAGGAGCAAGAAATCCCAAGACAGAAAGATCT	5399
Qy	5401	TCAGAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAATCTGCCACAGATCAACTGG	5460
Db	5400	TCAGAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAATCTGCCACAGATCAACTGG	5459
Qy	5461	AATGATATGCTACAGCTGTGTGTGCTTCTGTGTGTGAGAGACGTTTCATCATTCACCTTG	5520
Db	5460	AATGATATGCTACAGCTGTGTGTGCTTCTGTGTGTGAGAGACGTTTCATCATTCACCTTG	5519
Qy	5521	GCAACAGGTTCACACCCAAATGTTGGTGTGTCAGACAGATGCTCTGGACADAGGACATGGCT	5580
Db	5520	GCAACAGGTTCACACCCAAATGTTGGTGTGTCAGACAGATGCTCTGGACADAGGACATGGCT	5579
Qy	5581	TTCATATGCAATTTGGGACAGATGTGTAGGACACTGTGTGTGACCCGAGAGTGGGTGTGACA	5640
Db	5580	TTCATATGCAATTTGGGACAGATGTGTAGGACACTGTGTGTGACCCGAGAGTGGGTGTGACA	5639
Qy	5641	GTTAGACACTCTACACAGTGGCAGAGCTGGACACTTACCTGATATACCCAGATTCGCCACA	5700
Db	5640	GTTAGACACTCTCTACACAGTGGCAGAGCTGGACACTTACCTGATATACCCAGATTCGCCACA	5699
Qy	5701	GCACACTACTGA 5711	
Db	5700	GCACACTACTGA 5710	

Search completed: May 27, 1999, 10:21:29  
Job time: 10355 sec



GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: May 27, 1999, 20:03:07 ; Search time 360.2 Seconds  
(without alignments)  
2982.836 Million cell updates/sec

Title: US-08-798-691A-3

Perfect score: 5711  
Sequence: 1 AGCTCGCTGAGACTTCTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY\_NUC

Searched: 240622 seqs, 94065609 residues

Database: N\_Geneseq\_34:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5711	100.0	5914	1	T17493
2	5711	100.0	5711	1	V64449
3	5710.6	100.0	5711	1	V64463
4	5710.6	100.0	5711	1	V64458
5	5710.6	100.0	5711	1	V64458
6	5710.6	100.0	5711	1	V64459
7	5710.6	100.0	5711	1	V64460
8	5710.6	100.0	5711	1	V64461
9	5710.6	100.0	5711	1	V64462
10	5709.4	100.0	5914	1	T18310
11	5709.4	100.0	5914	1	T17438
12	5709.4	100.0	5914	1	T32601
13	5709.4	100.0	5712	1	T84840
14	5707.8	99.9	5914	1	T18311
15	5707.8	99.9	5914	1	T18313
16	5707.8	99.9	5914	1	T17445
17	5707.8	99.9	5914	1	T17445
18	5707.8	99.9	5914	1	T17449
19	5707.8	99.9	5914	1	T17453
20	5707.8	99.9	5914	1	T17457
21	5707.8	99.9	5914	1	T17462
22	5707.8	99.9	5914	1	T17466
23	5707.8	99.9	5914	1	T17468
24	5707.8	99.9	5914	1	T17471
25	5707.8	99.9	5914	1	T17476
26	5707.8	99.9	5914	1	T17478
27	5707.8	99.9	5914	1	T17479
28	5707.8	99.9	5914	1	T17481
29	5707.8	99.9	5914	1	T17483
30	5707.8	99.9	5914	1	T17484
31	5707.8	99.9	5914	1	T17486
32	5707.8	99.9	5914	1	T17489
33	5707.8	99.9	5914	1	T17490
34	5707.8	99.9	5914	1	T17491
35	5707.8	99.9	5914	1	T17492
36	5707.8	99.9	5914	1	T17494
37	5707.8	99.9	5914	1	T17495
38	5707.8	99.9	5914	1	T17496
39	5707.8	99.9	5914	1	T17497
40	5707.8	99.9	5914	1	T17498
41	5707.8	99.9	5914	1	T17499
42	5707.8	99.9	5914	1	T17500
43	5707.8	99.9	5914	1	T17501

44 5707.8 99.9 5914 1 T17502  
45 5707.8 99.9 5711 1 V60569

Mutated BRCA1 codi  
Tumourigenic BRCA1

## ALIGNMENTS

RESULT 1  
T17493 T17493 standard; cDNA; 5914 BP.  
AC T17493:  
DE 02-OCT-1996 (first entry)  
DE Mutated BRCA1 coding sequence from PM06.  
KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;  
KW antibody production; germline alteration; probe; lesion neoplasia; human;  
OS gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cds 120..5711  
FT mutation /tag= a  
FT /product= BRCA1 mutant  
FT 2731  
FT /tag= b  
FT /note= "C to T mutation"

W09605306-A2.  
PD 22-FEB-1996.  
PE 11-AUG-1995; U10202.  
PR 12-AUG-1994; US-289221.  
PR 02-SEP-1994; US-300266.  
PR 16-SEP-1994; US-308104.  
PR 29-NOV-1994; US-348824.  
PR 24-MAR-1995; US-409305.  
PR 07-JUN-1995; US-483553.  
PR 07-JUN-1995; US-480784.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (CANC-) CANCER INST.  
PA (RECH-) CENT RECH DU CHUL.  
PI Durocher F, Emi M, Nakamura Y, Simard J, Shattuck-Eidens DM;  
DR WPI; 96-139702/14.  
DR P-PSDB; R81535.  
PT New nucleic acid and polypeptide for mutant or polymorphic BRCA1  
PT gene - for diagnosis and therapy of human breast and ovarian cancer  
PT and for diagnosing pre-disposition to these cancers  
PS Claim 1; 218pp: English.  
CC T17435-T17453 and T17455-T17529 represent mutations of the human breast  
CC and ovarian cancer predisposing gene (BRCA1) (for wild type see T17438).  
CC proteins encoded by these mutations (see R81483-R81497 and R81499-R81546)  
CC can be used as immunogens for antibody production. These mutant BRCA1  
CC genes have at least 1 mutation or polymorphism in comparison to the wild  
CC type sequence. By detecting a germline alteration in the wild type BRCA1  
CC gene, a predisposition for breast and ovarian cancer can be diagnosed.  
CC In one method, BRCA1 mRNA isolated from a tissue sample from a subject  
CC has a probe, corresponding to a fragment of the wild type sequence (or an  
CC allele-specific probe for one of these mutations), added to it. The  
CC conditions allow for hybridisation of the probe to the mRNA, and any  
CC hybridisation which occurs is detected. Alternatively the BRCA1 gene in  
CC the tissue sample is isolated, and a shift in electrophoretic mobility of  
CC single stranded DNA from the sample on a non-denaturing polyacrylamide  
CC gel indicates a mutation. These methods of detection can also diagnose a  
CC lesion neoplasia associated with the BRCA1 locus. The methods may be  
CC used in gene therapy, protein replacement therapy and protein mimetics,  
CC and may be used to screen for drugs in cancer therapy.  
SQ Sequence 5914 BP; 2006 A; 1155 C; 1316 G; 1437 T;

Query Match 100.0%; Score 5711; DB 1; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCTGAGCCGACGAGCTGTGGGTTCTCAGATACTGGGCC 60  
DB 1 AGCTCGCTGAGACTTCTCTGAGCCGACGAGCTGTGGGTTCTCAGATACTGGGCC 60

OY	61	CTGGGCTCAGAGGCCCTTACCCTCTGCTCTGGGTAAAGTATTGGAACGAAAGAA	120
Db	61	CTGGGCTCAGAGGCCCTTACCCTCTGCTCTGGGTAAAGTATTGGAACGAAAGAA	120
OY	121	TGAGTTATCTGCTCTTCGCTTGAAGAGTAAATGCTATTATGCTATGACGAAA	180
Db	121	TGAGTTATCTGCTCTTCGCTTGAAGAGTAAATGCTATTATGCTATGACGAAA	180
OY	181	TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC	240
Db	181	TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC	240
OY	241	ACATTTTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCGAAGAAAGGCTTCAAGT	300
Db	241	ACATTTTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCGAAGAAAGGCTTCAAGT	300
OY	301	GTCCTTTATGTAAAGATGATTAACCAAAAAGAGCCCTACAGAAAGTACGAGTTATGTC	360
Db	301	GTCCTTTATGTAAAGATGATTAACCAAAAAGAGCCCTACAGAAAGTACGAGTTATGTC	360
OY	361	AACTTTGTGAAGAGCTATTTGAAAAATCATTTTGTGCTTTTCACTTGTGACACAGGTTTGA	420
Db	361	AACTTTGTGAAGAGCTATTTGAAAAATCATTTTGTGCTTTTCACTTGTGACACAGGTTTGA	420
OY	421	ATGCAACAGCTATTAATTTTGCAAAAAAGGAAATTAATCTCTGTAACTCTTAAAGATG	480
Db	421	ATGCAACAGCTATTAATTTTGCAAAAAAGGAAATTAATCTCTGTAACTCTTAAAGATG	480
OY	481	AAGTTCTATCATCCAAAGTATGGGCTACAGAAACGCTGCCAAACACTTCTACAGAGT	540
Db	481	AAGTTCTATCATCCAAAGTATGGGCTACAGAAACGCTGCCAAACACTTCTACAGAGT	540
OY	541	AAACCGAAAAATCCTTCTGTGAGGAAACCAAGTCTCAAGTGTCCAATCTCTAACTTTG	600
Db	541	AAACCGAAAAATCCTTCTGTGAGGAAACCAAGTCTCAAGTGTCCAATCTCTAACTTTG	600
OY	601	CTGTGAAACCTCTAGAGCAAAAGAGCGGATTAACAACCTCAAAAGAGCTGTCTACATG	660
Db	601	CTGTGAAACCTCTAGAGCAAAAGAGCGGATTAACAACCTCAAAAGAGCTGTCTACATG	660
OY	661	AATGGGATCTGATTTCTTCTGAAATATCCGTTAATTAAGGAACCTTTTTCAGTGTGGAG	720
Db	661	AATGGGATCTGATTTCTTCTGAAATATCCGTTAATTAAGGAACCTTTTTCAGTGTGGAG	720
OY	721	ATCAAGAAATTTGTTCAAAATCACCCTCAAGGAAACAGGAGTGAATCAATTTGGATTCTG	780
Db	721	ATCAAGAAATTTGTTCAAAATCACCCTCAAGGAAACAGGAGTGAATCAATTTGGATTCTG	780
OY	781	CAAAAAAGGCTGCTTGTGAATTTTCTGACGCGATGTAAACAAATACTGAACATCAAC	840
Db	781	CAAAAAAGGCTGCTTGTGAATTTTCTGACGCGATGTAAACAAATACTGAACATCAAC	840
OY	841	CCAGTAATTAATGATTGAACCAACGCTGAGAGGCTCAGCTGAGAGCTCCAGAAAGT	900
Db	841	CCAGTAATTAATGATTGAACCAACGCTGAGAGGCTCAGCTGAGAGCTCCAGAAAGT	900
OY	901	ATCAGGAGTAGTTCTGTTTCAAACTTCGATGTGAGCATGTGGCAACAAATFACTGTGCA	960
Db	901	ATCAGGAGTAGTTCTGTTTCAAACTTCGATGTGAGCATGTGGCAACAAATFACTGTGCA	960
OY	961	GCTCATTTACAGCATGAGACAGCAGTTTATTACTCACTAAAGCAAGATGATGTAGAA	1020
Db	961	GCTCATTTACAGCATGAGACAGCAGTTTATTACTCACTAAAGCAAGATGATGTAGAA	1020
OY	1021	AGGCTGAATTTCTGTATATATTAAGCAACAGCCTTGCTTAGCAAGAGCCAACTTAACAGAT	1080
Db	1021	AGGCTGAATTTCTGTATATATTAAGCAACAGCCTTGCTTAGCAAGAGCCAACTTAACAGAT	1080
OY	1081	GGGCTGAAGATTAAGGAACATGTATATGATGGGGAGCTCCACAGACAGAAAAAGGTAG	1140
Db	1081	GGGCTGAAGATTAAGGAACATGTATATGATGGGGAGCTCCACAGACAGAAAAAGGTAG	1140
OY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAATGAATGAAGCAAAATGCTCATCT	1200

Db	1141	ATCTGAATGCTGATCCCTCTGTGTAGGAAABAAATGAAATTAAGCAAGAACTGCCATGCT	1200
Qy	1201	CAGAAATACCTTAGAGATACAGTGAAGATCTTCTTGATTAACACTAAATPACACATTCAG	1260
Db	1201	CAGAAATACCTTAGAGATACAGTGAAGATCTTCTTGATTAACACTAAATPACACATTCAG	1260
Qy	1261	AAATTAATGAGTGGTTTCCAGAAATGATGTAAGTGTAGTCTGATGACTACATGATG	1320
Db	1261	AAATTAATGAGTGGTTTCCAGAAATGATGTAAGTGTAGTCTGATGACTACATGATG	1320
Qy	1321	GGGAGCTCGATCCAAATGCGCAAGTACTGATGATTTGGACGTTCTTAATGTAGATGATG	1380
Db	1321	GGGAGCTCGATCCAAATGCGCAAGTACTGATGATTTGGACGTTCTTAATGTAGATGATG	1380
Qy	1381	AAATATCTGTTCTTCAGAGAAATTAACATTAAGTGGCCAGTGTACTCTCATGAGGCTTTAA	1440
Db	1381	AAATATCTGTTCTTCAGAGAAATTAACATTAAGTGGCCAGTGTACTCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCCTCTCCAAATCAGTAGAGATTAATTTGAAGCAAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCCTCTCCAAATCAGTAGAGATTAATTTGAAGCAAAATAT	1500
Qy	1501	TTGGAAAACTATCCGGAAGAAGCAAGCCTCCCAACTTAAGCCATGTAACTGAATATC	1560
Db	1501	TTGGAAAACTATCCGGAAGAAGCAAGCCTCCCAACTTAAGCCATGTAACTGAATATC	1560
Qy	1561	TAAATATAGAGCAATTTGTTACTAGAGCAAGATTAATACAGAGCGTCCCTCACAAATA	1620
Db	1561	TAAATATAGAGCAATTTGTTACTAGAGCAAGATTAATACAGAGCGTCCCTCACAAATA	1620
Qy	1621	AATTAAGCCGTAAAAAGAGAGCACTACATCAGGCGTTTCATCCTGAGATTTTATCAAGAA	1680
Db	1621	AATTAAGCCGTAAAAAGAGAGCACTACATCAGGCGTTTCATCCTGAGATTTTATCAAGAA	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGATCTCTGAAATGTATAATGAGGAAGTAAACCAACAGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGATCTCTGAAATGTATAATGAGGAAGTAAACCAACAGGAGC	1740
Qy	1741	AGAAATGCTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT	1800
Db	1741	AGAAATGCTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT	1800
Qy	1801	CTATTCAGAAATGAGAAAAATCTTAACCAATAGAACTACTCGAAAAAAGATCTGCTTCA	1860
Db	1801	CTATTCAGAAATGAGAAAAATCTTAACCAATAGAACTACTCGAAAAAAGATCTGCTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTATTAAGACAGATTAAGCAATGTGAAGTCCGAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTATTAAGACAGATTAAGCAATGTGAAGTCCGAATTAATATCC	1920
Qy	1921	ACAATTCAAAAAGACCTTAAGAAATAGAGGTGAGAGAGTCTCTACACAGGCAATATTC	1980
Db	1921	ACAATTCAAAAAGACCTTAAGAAATAGAGGTGAGAGAGTCTCTACACAGGCAATATTC	1980
Qy	1981	ATGCGCTGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040
Db	1981	ATGCGCTGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040
Qy	2041	TTGATAGTGTCTTACGACATGTAAGAGATTAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Db	2041	TTGATAGTGTCTTACGACATGTAAGAGATTAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Qy	2101	GGCAGACAGAAACCTTACAACTATGGAAGGTTAAAGAACCTTCAACTGGAGCAAGAAGA	2160
Db	2101	GGCAGACAGAAACCTTACAACTATGGAAGGTTAAAGAACCTTCAACTGGAGCAAGAAGA	2160
Qy	2161	GTAACAAGCCAAATGAACACAGCAAGTAAAGACATGACGCGATCTTCCAGAGCGTGA	2220
Db	2161	GTAACAAGCCAAATGAACACAGCAAGTAAAGACATGACGCGATCTTCCAGAGCGTGA	2220
Qy	2221	AGTTAAACAAATGACCTGCTTCTTCTTAATGATGATGATGATGATGATGATGATGATGAT	2280

D	2221	AGTTAACAAATGCACCGTGGTCTTTTACTAAGTGTTCAAAATACCACTGACTTAAGAT	2280
Q	2281	TTGTCAATCCTAGCCTTCCAGAGAAAGAAAAAGAAAGAACTAGAAAAGTTAAAGTG	2340
D	2281	TTGTCAATCCTAGCCTTCCAGAGAAAGAAAAAGAAAGAACTAGAAAAGTTAAAGTG	2340
Q	2341	CTATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGGACAAAAGGTTTTCAACTG	2400
D	2341	CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGGACAAAAGGTTTTCAACTG	2400
Q	2401	AAAGATCTGAGAGAGTAGAGATTTTCATTTGGTACTGCTACTGATTAATGAGCACTAGG	2460
D	2401	AAAGATCTGAGAGAGTAGAGATTTTCATTTGGTACTGCTACTGATTAATGAGCACTAGG	2460
Q	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATAAT	2520
D	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAACAGAACCAATAAT	2520
Q	2521	GTCGATCTAGTGTGCAGCAATTTGAAAACCCCAAGGACTAATTATGTTGTTCCAAAG	2580
D	2521	GTCGATCTAGTGTGCAGCAATTTGAAAACCCCAAGGACTAATTATGTTGTTCCAAAG	2580
Q	2581	ATATTAATAATGACACAGAAAGGCTTTAAGTATCCATTTGGACATGATAGTTAACCACTC	2640
D	2581	ATATTAATAATGACACAGAAAGGCTTTAAGTATCCATTTGGACATGATAGTTAACCACTC	2640
Q	2641	GGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATCCTCAGTATTTGCGAATACAT	2700
D	2641	GGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATCCTCAGTATTTGCGAATACAT	2700
Q	2701	TCAAAGTTTCAAAGCGCCAGCTCATTTGCTGTGTTTCAAATCCAGGAAATGCGAAGAGG	2760
D	2701	TCAAAGTTTCAAAGCGCCAGCTCATTTGCTGTGTTTCAAATCCAGGAAATGCGAAGAGG	2760
Q	2761	AATGTGCAACATCTCTGCCCACTCTGGGCGCTTAAGAAACAAAGTCCAAAAGCACTT	2820
D	2761	AATGTGCAACATCTCTGCCCACTCTGGGCGCTTAAGAAACAAAGTCCAAAAGCACTT	2820
Q	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAGATAGTCTAATATCAAGCCTGTAC	2880
D	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAGATAGTCTAATATCAAGCCTGTAC	2880
Q	2881	AGACAGTTAATATCACTGCGAGGCTTTCCTGTGTGTGTCAGAAAGATAGCCAGTTGATA	2940
D	2881	AGACAGTTAATATCACTGCGAGGCTTTCCTGTGTGTGTCAGAAAGATAGCCAGTTGATA	2940
Q	2941	ATGCGAATGTAGATCAAAAGAGGCGCTAAGGTTTGTCTATCACTCAGTTCCAGAGCA	3000
D	2941	ATGCGAATGTAGATCAAAAGAGGCGCTAAGGTTTGTCTATCACTCAGTTCCAGAGCA	3000
Q	3001	ACGAACTGAGCTATCTACTCCAAATTAACATGSACTTTTACAAAACCCATATCGTATAC	3060
D	3001	ACGAACTGAGCTATCTACTCCAAATTAACATGSACTTTTACAAAACCCATATCGTATAC	3060
Q	3061	CACCACCTTTCCCATCAAGTCAATTTGTTTAAACTAATGTAGAAAAAATCTGCTAGAG	3120
D	3061	CACCACCTTTCCCATCAAGTCAATTTGTTTAAACTAATGTAGAAAAAATCTGCTAGAG	3120
Q	3121	AAAACCTTGGAGGAACATTCAAATCTCACCTGAGAAAGAAATGGGAATGAGAACTTCCAA	3180
D	3121	AAAACCTTGGAGGAACATTCAAATCTCACCTGAGAAAGAAATGGGAATGAGAACTTCCAA	3180
Q	3181	GTCAGTGCACAAATTTAGCGCGTATATACATTAGAGAAAATTTTATTAAGAGCCAGCT	3240
D	3181	GTCAGTGCACAAATTTAGCGCGTATATACATTAGAGAAAATTTTATTAAGAGCCAGCT	3240
Q	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
D	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Q	3301	TAGTTCCTAGTGAATGAATATTCACAGCAGAACTAGGTGAAAACAGAGGCCAAATTTGA	3360
D	3301	TAGTTCCTAGTGAATGAATATTCACAGCAGAACTAGGTGAAAACAGAGGCCAAATTTGA	3360

QY	3361	ATNTATGCTAGATTGGGGTTTTCGAACCGTAGGCTATTAACAAGCTCTCTCGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTCGAACCTGAGGCTATTAACAAGCTCTCTCGAA	3420
QY	3421	GTAATTGTAAGCACTCGGAATATAAAAAGCAAGAAATATMAAGTAGTGCAGCTGTTA	3480
Db	3421	GTAATTGTAAGCACTCGGAATATAAAAAGCAAGAAATATMAAGTAGTGCAGCTGTTA	3480
QY	3481	ATACAGATTTCCTCCATATCTGATTTACAGATPACTTAGAACGCTTATGGAGTAGTC	3540
Db	3481	ATACAGATTTCCTCCATATCTGATTTACAGATPACTTAGAACGCTTATGGAGTAGTC	3540
QY	3541	ATGCATCTCAGGTTTGTTCGAGACACCGATACCTGTAGATCATGCTGGTAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTTCGAGACACCGATACCTGTAGATCATGCTGGTAATTAAGG	3600
QY	3601	AAGATPACTAGTTTGTGTAATGACATTAGAAAGTTCTGCTGTTTTAGCAAAACGG	3660
Db	3601	AAGATPACTAGTTTGTGTAATGACATTAGAAAGTTCTGCTGTTTTAGCAAAACGG	3660
QY	3661	TCCGAAAGGAGGAGCTTAGAGAGAGTCAGGCCCTTACCCATACATTTGGCTCAGG	3720
Db	3661	TCCGAAAGGAGGAGCTTAGAGAGAGTCAGGCCCTTACCCATACATTTGGCTCAGG	3720
QY	3721	GTTACCGAAGGGGGCCCAAAATTTAGAGTCTCAGAAAGAACTTATCTAGTAGATG	3780
Db	3721	GTTACCGAAGGGGGCCCAAAATTTAGAGTCTCAGAAAGAACTTATCTAGTAGATG	3780
QY	3781	AAGAGCTTCCTGCTTCCAAACACTGTTATTTGGTAAAGTAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCTGCTTCCAAACACTGTTATTTGGTAAAGTAACAATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCAATAGACCGCTGTACCGAGTGTCTCTAGAACACAGAGGAGATTTAT	3900
Db	3841	CTACTAGGCAATAGACCGCTGTACCGAGTGTCTCTAGAACACAGAGGAGATTTAT	3900
QY	3901	TATCATTTGAAGATAGCTTAATGATGACTGCAGTAACCAAGTAATTTGGCAAGGCATCTC	3960
Db	3901	TATCATTTGAAGATAGCTTAATGATGACTGCAGTAACCAAGTAATTTGGCAAGGCATCTC	3960
QY	3961	AGGAACCAACACTTAGTAGAGAGAAACAAATGTTCTGAGCTGTTTCTTCAACAGTCA	4020
Db	3961	AGGAACCAACACTTAGTAGAGAGAAACAAATGTTCTGAGCTGTTTCTTCAACAGTCA	4020
QY	4021	GTTGATTTGGAAGACTTGACATGCAAAATATCAACACCCAGGATCCTTCTTGTGATTGGTCTT	4080
Db	4021	GTTGATTTGGAAGACTTGACATGCAAAATATCAACACCCAGGATCCTTCTTGTGATTGGTCTT	4080
QY	4081	CCAAACAAATGAGGCAATCACTCTGAAAAGCAGAGGATTTGCTGTAGTATCAAGGAATTTGG	4140
Db	4081	CCAAACAAATGAGGCAATCACTCTGAAAAGCAGAGGATTTGCTGTAGTATCAAGGAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAAAAATATATCAAGAGCAAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAAAAATATATCAAGAGCAAAAGCA	4200
QY	4201	TGGAATCAAACTTAGTGGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAAG	4260
Db	4201	TGGAATCAAACTTAGTGGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAAG	4260
QY	4261	ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACCTAGAGAGGGGATTCACATGC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACCTAGAGAGGGGATTCACATGC	4320
QY	4321	AACATTAACCTGATTAAGCTTCACAGACGAATAGGCTGAATAGAACCTGTGTAGAACAGC	4380
Db	4321	AACATTAACCTGATTAAGCTTCACAGACGAATAGGCTGAATAGAACCTGTGTAGAACAGC	4380
QY	4381	ATGGGAGCCAGGCTTCTTAACAGGTACCCCTTCATATAGTAGTACTTCTGCTCGTAGG	4440
Db	4381	ATGGGAGCCAGGCTTCTTAACAGGTACCCCTTCATATAGTAGTACTTCTGCTCGTAGG	4440

```

QY 4441 ACCGCGAATCCAGAACAAAGCATCAGAAAAAGCATTAATCTACAGAAAAAGTA 4500
DB 4441 ACCGCGAATCCAGAACAAAGCATCAGAAAAAGCATTAATCTACAGAAAAAGTA 4500
QY 4501 GTGAATACCCATTAAGCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTTGAGGTCTG 4560
DB 4501 GTGAATACCCATTAAGCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTTGAGGTCTG 4560
QY 4561 CAGATAGTTTACAGAGTAAATAAAGAACAGAGAGTGAAGAGTTCATCCCTCTTAAT 4620
DB 4561 CAGATAGTTTACAGAGTAAATAAAGAACAGAGAGTGAAGAGTTCATCCCTCTTAAT 4620
QY 4621 GCGCATATTAGATGATAGTGTGTGATGACACAGTGTCTGTGGAGTCTTCAAGATAGA 4680
DB 4621 GCGCATATTAGATGATAGTGTGTGATGACACAGTGTCTGTGGAGTCTTCAAGATAGA 4680
QY 4681 ACTACCATCTCAAGAGAGAGTCTTAAGTTGATGTGGAGAGCAACAGCTGGAG 4740
DB 4681 ACTACCATCTCAAGAGAGAGTCTTAAGTTGATGTGGAGAGCAACAGCTGGAG 4740
QY 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800
DB 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGATCTGGATTCAGCCTCTTCTGTGATGACCTGATCTGATCTCTG 4860
DB 4801 CCCCTTACCTGGATCTGGATTCAGCCTCTTCTGTGATGACCTGATCTGATCTCTG 4860
QY 4861 AAGACAGAGCCCGCAGAGTCAAGTCTGTGGACACATACATCTTCAACCTCTGATGA 4920
DB 4861 AAGACAGAGCCCGCAGAGTCAAGTCTGTGGACACATACATCTTCAACCTCTGATGA 4920
QY 4921 AAGTCCCAATTGAAGTTGACAGATCTGCCAGAGTCCAGCTGCTGCTACTG 4980
DB 4921 AAGTCCCAATTGAAGTTGACAGATCTGCCAGAGTCCAGCTGCTGCTACTG 4980
QY 4981 ATACTGGGTATTAATGACATGGAAGTGTGAGAGGAGAGCAACCAATTTGACAG 5040
DB 4981 ATACTGGGTATTAATGACATGGAAGTGTGAGAGGAGAGCAACCAATTTGACAG 5040
QY 5041 CTTCACAGAAAGGCTCAACAAAAAATGTCATGTGTGCTGCTGACCCAGAG 5100
DB 5041 CTTCACAGAAAGGCTCAACAAAAAATGTCATGTGTGCTGCTGACCCAGAG 5100
QY 5101 AATTATGCTGTGTGACAGATTTGCCAGAAAAACCAACATCATCTTAATCTAATTA 5160
DB 5101 AATTATGCTGTGTGACAGATTTGCCAGAAAAACCAACATCATCTTAATCTAATTA 5160
QY 5161 CTGAAGAGACTACTCATGTGTGTAAGACATGCTGAGTGTGTGTAAGGAGAC 5220
DB 5161 CTGAAGAGACTACTCATGTGTGTAAGACATGCTGAGTGTGTGTAAGGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGTAGTAGTATTTTGGGTGACC 5280
DB 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGTAGTAGTATTTTGGGTGACC 5280
QY 5281 AGCTATTTAAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340
DB 5281 AGCTATTTAAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAAGAGATGTG 5340
QY 5341 TCAATGGAAGAAACCAAGAGTCCAAAGGAGAGCAAGATCCCAAGAGCAAGAGATCT 5400
DB 5341 TCAATGGAAGAAACCAAGAGTCCAAAGGAGAGCAAGATCCCAAGAGCAAGAGATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTGTATGAGCCCTTCAACCAATCTCCACAGATCAATG 5460
DB 5401 TCAGGGGGCTAGAAATCTGTGTATGAGCCCTTCAACCAATCTCCACAGATCAATG 5460
QY 5461 AATGATGCTACAGCTGTGTGTCTGTGTGTGAAGAGCTTTCATCTACCTTG 5520
DB 5461 AATGATGCTACAGCTGTGTGTGTGTGTGTGTGAAGAGCTTTCATCTACCTTG 5520
QY 5521 GCACAGGTGTCCACCAATTTGTGTGTGTGACGACAGATGCTGACAGAGACATGGCT 5580

```

```

DB 5521 GCACAGGTGTCCACCAATTTGTGTGTGTGACGACAGATGCTGACAGAGACATGGCT 5580
QY 5581 TCATATGATTTGGGAGATGTGTGAGGACACTGTGTGACCCGAGAGTGGTGTGACA 5640
DB 5581 TCATATGATTTGGGAGATGTGTGAGGACACTGTGTGACCCGAGAGTGGTGTGACA 5640
QY 5641 GTGTAGCACTTACAGATGCGAGAGAGTGGACACCTACTGATTAACCCAGATCCCA 5700
DB 5641 GTGTAGCACTTACAGATGCGAGAGAGTGGACACCTACTGATTAACCCAGATCCCA 5700
QY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711

RESULT 2
V46449
ID V46449 standard; cDNA: 5711 BP.
AC V46449;
DT 18-NOV-1998 (first entry)
DE Human BRCA1: om12 cDNA.
KW BRCA1: om12: human: breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q: ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..5711
FT /tag= a
FT /product= "BRCA1 om12 protein"
PN US5750400-A.
PD 12-MAY-1998.
PF 12-FEB-1997: 798691.
PR 12-FEB-1996: US-598591.
PR 12-FEB-1997: US-798691.
PA (ONCO-) ONCORMED INC.
PI Allen AC, Alvares CP, Cultz BS, Murphy PD, Olson SJ,
PI Schelter DB, Zeng B;
DR WPI: 98-296774/26.
DR P-PSDB: W76099.
PT BRCA1 om1 gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
PS Claim 2d: Column 41-46: 54pp; English.
CC This sequence encodes the human BRCA1 (breast and ovarian cancer
CC predisposing gene) om12 gene. This sequence and polymorphic variations of
CC this sequence are useful for the identification of an individual who may
CC or may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers.
SQ Sequence 5711 bp: 1956 A; 1098 C; 1274 G; 1383 T;

Query Match 100.0%; Score 5711; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGTTTCTCAGATACTGGCC 60
DB 1 AGCTGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGTTTCTCAGATACTGGCC 60
QY 61 CTGCGCTCAGAGAGGCTTACCTCTGCTGTGGTAAGTTCATTGGAACAGAAAGAA 120
DB 61 CTGCGCTCAGAGAGGCTTACCTCTGCTGTGGTAAGTTCATTGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTTCCGCTTGAAGAGTACAAATGCTATTAATGATGCAAGAAA 180
DB 121 TGGATTATCTGCTTCCGCTTGAAGAGTACAAATGCTATTAATGATGCAAGAAA 180

```





Db 2341 CTAATTAATGCTAAGACCCCAAGATCTCATGTTAAGTGGAGAAGGTTTCCAACTG 2400  
Qy 2401 AAGATCTGTAGAGATGACAGTATTTCAATTTGGTACTGTGATGATGAGCACTAG 2460  
Db 2401 AAGATCTGTAGAGATGACAGTATTTCAATTTGGTACTGTGATGATGAGCACTAG 2460  
Qy 2461 AAGATCTGTAGAGATGACAGTATTTCAATTTGGTACTGTGATGATGAGCACTAG 2520  
Db 2461 AAGATCTGTAGAGATGACAGTATTTCAATTTGGTACTGTGATGATGAGCACTAG 2520  
Qy 2521 GTGTAGTACGTGTGAGATTTGAAACCCCAAGGACTAATTCAGTGTGTTCCAAAG 2580  
Db 2521 GTGTAGTACGTGTGAGATTTGAAACCCCAAGGACTAATTCAGTGTGTTCCAAAG 2580  
Qy 2581 ATAAATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGACATGAAGTTAACACAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGACATGAAGTTAACACAGTC 2640  
Qy 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAATGATGCTCATGTTTGGCAGAAATACAT 2700  
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAATGATGCTCATGTTTGGCAGAAATACAT 2700  
Qy 2701 TCAAGGTTTCAAGGGCCGCTGATTTGCTGTTTCAATCCAGAAATGCGAAGAG 2760  
Db 2701 TCAAGGTTTCAAGGGCCGCTGATTTGCTGTTTCAATCCAGAAATGCGAAGAG 2760  
Qy 2761 AATGTGCAACATCTCTGCCCCACTGCGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCCCCACTGCGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAGAAATCAAGGAAAGATGATATATCAAGCCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAGAAATCAAGGAAAGATGATATATCAAGCCCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGAGGCTTCTGTTGTTGCTGAGAAAGATGAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTTGTTGCTGAGAAAGATGAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTATGATCAAGAGAGCTGAGTTTGTCTATCATCTCAGTTGAGAGCA 3000  
Db 2941 ATGCCAAATGTATGATCAAGAGAGCTGAGTTTGTCTATCATCTCAGTTGAGAGCA 3000  
Qy 3001 AGGAACGAGACTCATCTTCCAAATTAACATGAGACTTTACAAACCCATATCGATAC 3060  
Db 3001 AGGAACGAGACTCATCTTCCAAATTAACATGAGACTTTACAAACCCATATCGATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTGAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTGAAGAAATCTGCTAGAG 3120  
Qy 3121 AAACTTTGAGGACATTCATATGTCACCTGAAAGAGAAATGGAAATGGAACATTCGA 3180  
Db 3121 AAACTTTGAGGACATTCATATGTCACCTGAAAGAGAAATGGAAATGGAACATTCGA 3180  
Qy 3181 GTACAGTAGACATTTAGCCGCTAATTAATGAGAAATGTTTTTAAAGAACCCAGCT 3240  
Db 3181 GTACAGTAGACATTTAGCCGCTAATTAATGAGAAATGTTTTTAAAGAACCCAGCT 3240  
Qy 3241 CAAGCAATATTAAAGAGAGTTCAGACTAATGAATGAGTGGGCTCCAGTATTAAGAAA 3300  
Db 3241 CAAGCAATATTAAAGAGAGTTCAGACTAATGAATGAGTGGGCTCCAGTATTAAGAAA 3300  
Qy 3301 TAGGTTCCAGTATGATGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 3360  
Db 3301 TAGGTTCCAGTATGATGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 3360  
Qy 3361 ATGCTATGCTATGATTTAGGGGTTTGGCAACCTGAGGCTTATTAACAAATCTTCCGGA 3420  
Db 3361 ATGCTATGCTATGATTTAGGGGTTTGGCAACCTGAGGCTTATTAACAAATCTTCCGGA 3420  
Qy 3421 GTAATTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480  
Db 3421 GTAATTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480

Db 3421 GTAATTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAAGAACAGCCTATGGGAATGAC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAAGAACAGCCTATGGGAATGAC 3540  
Qy 3541 ATGATCTAGAGTTGTTGTGAGACACCTGATGAGTGTGATGATGATGATGATGATG 3600  
Db 3541 ATGATCTAGAGTTGTTGTGAGACACCTGATGAGTGTGATGATGATGATGATGATG 3600  
Qy 3601 AAGATCTAGTTTGTGCTGAAATGACATTAAGGAAGTGTGCTGTTTAAAGAAAGCG 3660  
Db 3601 AAGATCTAGTTTGTGCTGAAATGACATTAAGGAAGTGTGCTGTTTAAAGAAAGCG 3660  
Qy 3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGGCTTTCACCCATACACATTTGGCTCAG 3720  
Db 3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGGCTTTCACCCATACACATTTGGCTCAG 3720  
Qy 3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACCTTATAGTAGATG 3780  
Db 3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACCTTATAGTAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy 3841 CTAATAGGATAGACACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGATTTAT 3900  
Db 3841 CTAATAGGATAGACACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGATTTAT 3900  
Qy 3901 TATCATGGAAGATAGCTTAAATGATGATGATGATGATGATGATGATGATGATGATG 3960  
Db 3901 TATCATGGAAGATAGCTTAAATGATGATGATGATGATGATGATGATGATGATGATG 3960  
Qy 3961 AGGAACATCACCTTGTAGAGAGAAACAAATGTTGCTGAGCTGTTTCTTCAACAGTGA 4020  
Db 3961 AGGAACATCACCTTGTAGAGAGAAACAAATGTTGCTGAGCTGTTTCTTCAACAGTGA 4020  
Qy 4021 GTGAATTTGGAAGACTTGAATGATGATGATGATGATGATGATGATGATGATGATG 4080  
Db 4021 GTGAATTTGGAAGACTTGAATGATGATGATGATGATGATGATGATGATGATGATG 4080  
Qy 4081 CCAAAACAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140  
Db 4081 CCAAAACAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140  
Qy 4141 TTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
Db 4141 TTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4200  
Qy 4201 TGGATTTCAAACTTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATG 4260  
Db 4201 TGGATTTCAAACTTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATG 4260  
Qy 4261 TGGATTTCAAACTTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATG 4320  
Db 4261 TGGATTTCAAACTTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATG 4320  
Qy 4321 AACATTAACCTGATTAAGTTCAGAGAGAAATGCTGAATCTGAAGCTGTGTAAGAGC 4380  
Db 4321 AACATTAACCTGATTAAGTTCAGAGAGAAATGCTGAATCTGAAGCTGTGTAAGAGC 4380  
Qy 4381 ATGGAGGAGGAGCTTCTAAGAGTACCTTCCATATGATGATGATGATGATGATGATG 4440  
Db 4381 ATGGAGGAGGAGCTTCTAAGAGTACCTTCCATATGATGATGATGATGATGATGATG 4440  
Qy 4441 ACCTGCGAAATCCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4500  
Db 4441 ACCTGCGAAATCCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4500  
Qy 4501 GTGAATTAACCTTATTAAG 4560  
Db 4501 GTGAATTAACCTTATTAAG 4560

QY	4561	CAGAAATCTTACCACATAAAAAAAGAACCCAGAGAGTGGAAAGGTGCATCCCTCTCTAAT	4620
Db	4561	CAGATATCTTACCACATAAAAAAAGAACCCAGAGAGTGGAAAGGTGCATCCCTCTCTAAT	4620
QY	4621	GCCCATCATAGATGATAGGTGGTACATCAGAGTATGCTGGAGTCTTCAGATAAGAA	4680
Db	4621	GCCCATCATAGATGATAGGTGGTACATCAGAGTATGCTGGAGTCTTCAGATAAGAA	4680
QY	4681	ACTACCATCTCAAGAGAGACTCATTTAAGGTTGTTGATGTGAGGAGCAGACAGCTGGAAG	4740
Db	4681	ACTACCATCTCAAGAGAGAGCTCATTTAAGGTTGTTGATGTGAGGAGCAGACAGCTGGAAG	4740
QY	4741	AGCTGGGGCCACAGATTTGAGGAAACATCTACTTGGCCAAAGGCAACATCTAAGGGAA	4800
Db	4741	AGCTGGGGCCACAGATTTGAGGAAACATCTACTTGGCCAAAGGCAACATCTAAGGGAA	4800
QY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTCTCTCTGATGACCCCTGAATCTGATCCTCTG	4860
Db	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTCTCTCTGATGACCCCTGAATCTGATCCTCTG	4860
QY	4861	AAGACAGAGCCCAAGACTCAGCCCTGTTGGGAACAATACATCTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGAGCCCAAGACTCAGCCCTGTTGGGAACAATACATCTTCAACCTCTGATTTGA	4920
QY	4921	AAGTCCCCCAATTTGAAGTTGACGAATCTGCCAGAGTCCAGACTCTGCTCATACTACTG	4980
Db	4921	AAGTCCCCCAATTTGAAGTTGACGAATCTGCCAGAGTCCAGACTCTGCTCATACTACTG	4980
QY	4981	ATATCTGCTGGGTATATTCGAATGGAAAGAAAGTGTAGCAGGGAGAACCCAGAAATTGACAG	5040
Db	4981	ATATCTGCTGGGTATATTCGAATGGAAAGAAAGTGTAGCAGGGAGAACCAAAATTGACAG	5040
QY	5041	CTTCAACAGAAAGGATCAACAAAGAAATGTCATGGTGGTGTCTGGCTGAGCCCAAGAG	5100
Db	5041	CTTCAACAGAAAGGATCAACAAAGAAATGTCATGGTGGTGTCTGGCTGAGCCCAAGAG	5100
QY	5101	AAATTATGCTGTGTACAAAGTTTCCAGAAAACCCACATCACTTTAACTAATCTAATTA	5160
Db	5101	AAATTATGCTGTGTACAAAGTTTCCAGAAAACCCACATCACTTTAACTAATCTAATTA	5160
QY	5161	CTGGAAGAGACTACTCATGTTGTATGAAAGAAACAGATGCTGAGTTTGTGTGAAGGGACAC	5220
Db	5161	CTGGAAGAGACTACTCATGTTGTATGAAAGAAACAGATGCTGAGTTTGTGTGAAGGGACAC	5220
QY	5221	TGAATATTTTCTAGAGAAATGCGGGAGGAAATGGTATGATTTAGCTAATTTCTGGGTGACCC	5280
Db	5221	TGAATATTTTCTAGAGAAATGCGGGAGGAAATGGTATGATTTAGCTAATTTCTGGGTGACCC	5280
QY	5281	AGTCTATTTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTAACTCAGAGAGAGTGTGG	5340
Db	5281	AGTCTATTTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTAACTCAGAGAGAGTGTGG	5340
QY	5341	TCATATGGAAGAAACCCACCAAGGTCCTCAACCGAGCAAGAGAAATCCCAAGACAGAAAGATCT	5400
Db	5341	TCATATGGAAGAAACCCACCAAGGTCCTCAACCGAGCAAGAGAAATCCCAAGACAGAAAGATCT	5400
QY	5401	TCAAGGGGCTAGAAATCTGTGCTATGGGCTTCAACCAACATGTGCCACAGATCAACTGG	5460
Db	5401	TCAAGGGGCTAGAAATCTGTGCTATGGGCTTCAACCAACATGTGCCACAGATCAACTGG	5460
QY	5461	AATGAGATGTCAGAGCTGTGGGGCTTCTGTGTGAAGAGCTTTCATCATCTTACACCTTG	5520
Db	5461	AATGAGATGTCAGAGCTGTGGGGCTTCTGTGTGAAGAGCTTTCATCATCTTACACCTTG	5520
QY	5521	GCACAGGTGTCCACCAATTTGTGGTGTGTGTCACAGATGCTTGACAGAGCAATGGCT	5580
Db	5521	GCACAGGTGTCCACCAATTTGTGGTGTGTGTCACAGATGCTTGACAGAGCAATGGCT	5580
QY	5581	TCATATGCAATTTGGGCGAGATGTGTGAGGCAACCTGTGTGACCCCGAAGTGGGTGTTGGACA	5640
Db	5581	TCATATGCAATTTGGGCGAGATGTGTGAGGCAACCTGTGTGACCCCGAAGTGGGTGTTGGACA	5640

Query Match	Best Local Similarity	Matches 5710: Conservative	100.0%; Score 5710.6; DB 1; Length 5711; 100.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
0Y	1	AGCGCGGAGACCTCCGCGAACCCCGACCAAGCGCTGGGGTTCTCGAGTAACGTGGGCC	60
Db	1	AGCTGCGTGAAGCTCCGCGAACCCCGACCAAGCGCTGGGGTTCTCGAGTAACGTGGGCC	60
0Y	61	CTGGCGCTCAGGAGGCGCTTCAACCTCTGCTGGGTAAGTTCATTGGAAGAAAGAAA	120
Db	61	CCTGGCGCTCAGGAGGCGCTTCAACCTCTGCTGGGTAAGTTCATTGGAAGAAAGAAA	120
0Y	121	TGAGTTATTCCTGCTCTTGGCGGTGAAGAAGTACAAATGTCATTATAGCTTATGCGAATA	180
Db	121	TGAGTTATTCCTGCTCTTGGCGGTGAAGAAGTACAAATGTCATTATAGCTTATGCGAATA	180

Qy	181	TCCTTAAGTGTCCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCACCAAGTGTAC	240
Dy	181	TCCTTAAGTGTCCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCACCAAGTGTAC	240
Qy	241	ACATATTTTGCATTTTGGATGCTGGAACCTTCCAAACGAGAAAGAGGCTTCACAGT	300
Dy	241	ACATATTTTGCATTTTGGATGCTGGAACCTTCCAAACGAGAAAGAGGCTTCACAGT	300
Qy	301	GTCCCTTAATGTAAAGATGATATAAACCAAAAGAGAGCTTCAAGAAAGTACGAGATTAGTC	360
Dy	301	GTCCCTTAATGTAAAGATGATATAAACCAAAAGAGAGCTTCAAGAAAGTACGAGATTAGTC	360
Qy	361	AACTTGTGAAGAGCTATTGAAATTCATTTTGTCTTTCAGCTTGACACAGTTTGGAGT	420
Dy	361	AACTTGTGAAGAGCTATTGAAATTCATTTTGTCTTTCAGCTTGACACAGTTTGGAGT	420
Qy	421	ATGCAAAACAGCTTAATTTTGGCAAAAAAGAAAAATACCTCTCTAATCTCTAAAAAGATG	480
Dy	421	ATGCAAAACAGCTTAATTTTGGCAAAAAAGAAAAATACCTCTCTAATCTCTAAAAAGATG	480
Qy	481	AACTTCTATCATCCAAAGATGGGCTACAGAAAACGTCGCCAAAAGACTTCTACAGAGTG	540
Dy	481	AACTTCTATCATCCAAAGATGGGCTACAGAAAACGTCGCCAAAAGACTTCTACAGAGTG	540
Qy	541	AAACCCAAAATCCTTCTTCTGAGAAAACAGCTCTCAGTGTCCAACTCTCTAACCTTGGAA	600
Dy	541	AAACCCAAAATCCTTCTTCTGAGAAAACAGCTCTCAGTGTCCAACTCTCTAACCTTGGAA	600
Qy	601	CTGTGGAAGACTCTGAGACAAAGCAGGAGATACAACCTCAAAAGAGCTGTGCTACATG	660
Dy	601	CTGTGGAAGACTCTGAGACAAAGCAGGAGATACAACCTCAAAAGAGCTGTGCTACATG	660
Qy	661	AAATGGGATCTGATTTCTTCTGAAGATACCGTTTAATGAAGCAACTTATTGCAGTGTGGAG	720
Dy	661	AAATGGGATCTGATTTCTTCTGAAGATACCGTTTAATGAAGCAACTTATTGCAGTGTGGAG	720
Qy	721	ATCAAAATTTGTACAAATACACCCCTCAAGAACCAAGGATGAAATCAGTTTGGATCTG	780
Dy	721	ATCAAAATTTGTACAAATACACCCCTCAAGAACCAAGGATGAAATCAGTTTGGATCTG	780
Qy	781	CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGTGTAAACAAATCTAATCATCATC	840
Dy	781	CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGTGTAAACAAATCTAATCATCATC	840
Qy	841	CCAGTAATAATGATTTTGAACACCACTAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAAT	900
Dy	841	CCAGTAATAATGATTTTGAACACCACTAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAAT	900
Qy	901	ATCAGGCTAGTCTGTCTTTCACAACTGTCAGATGTGGACCATGTGGCAAAATCTCATGCCA	960
Dy	901	ATCAGGCTAGTCTGTCTTTCACAACTGTCAGATGTGGACCATGTGGCAAAATCTCATGCCA	960
Qy	961	GCTCATTTACAGCATGTAGAACACAGCGTTTATTACTCACTAAAGACAGATGTATGAAA	1020
Dy	961	GCTCATTTACAGCATGTAGAACACAGCGTTTATTACTCACTAAAGACAGATGTATGAAA	1020
Qy	1021	AGGCTGAATTTCTGTAATTAAGCAAAACAGCGCTGCTTAGCAAGAGGCCAACATACAGAT	1080
Dy	1021	AGGCTGAATTTCTGTAATTAAGCAAAACAGCGCTGCTTAGCAAGAGGCCAACATACAGAT	1080
Qy	1081	GGGCTTGAAGTAAAGAAACATGTATATATAGGGAGCTCCAGCAGACAGAAAAAGGTAG	1140
Dy	1081	GGGCTTGAAGTAAAGAAACATGTATATATAGGGAGCTCCAGCAGACAGAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCGCTGTGAGAGAAAAAGAAATGGAATAACAGAAACTGCCATGCT	1200
Dy	1141	ATCTGAATGCTGATCCCGCTGTGAGAGAAAAAGAAATGGAATAACAGAAACTGCCATGCT	1200
Qy	1201	CAGAGATCCTAAGATACTAGAGATGTCTCTTGATTAACCTAAATGTAGCATTTGACA	1260
Dy	1201	CAGAGATCCTAAGATACTAGAGATGTCTCTTGATTAACCTAAATGTAGCATTTGACA	1260
Qy	1261	AAATTAATAGTGTGTTTCCAGAAAGTGAATGTAAGTGTCTGTGATGACTCACATGATG	1320
Dy	1261	AAATTAATAGTGTGTTTCCAGAAAGTGAATGTAAGTGTCTGTGATGACTCACATGATG	1320
Qy	1321	GGAGCTGGAATCAATATGCACAAAGTGAATGTATTTGGAGCTTCTAAATGATGATGATG	1380
Dy	1321	GGAGCTGGAATCAATATGCACAAAGTGAATGTATTTGGAGCTTCTAAATGATGATGATG	1380
Qy	1381	AAATATTCGTGTTCTTCAGAGAAATATAGACTTACTGGCCAGTATCTCATAGGCTTTAA	1440
Dy	1381	AAATATTCGTGTTCTTCAGAGAAATATAGACTTACTGGCCAGTATCTCATAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTCTCTCCAAATCTGTAGAGATATTTGAAGCAAAATAT	1500
Dy	1441	TATGTAAAGTGAAGAGTCTCTCCAAATCTGTAGAGATATTTGAAGCAAAATAT	1500
Qy	1501	TTGGAAAAACCTATGGAAGAAAGGAGAGCTTCCCAACTTAAAGCCATGTAACGAAAAATC	1560
Dy	1501	TTGGAAAAACCTATGGAAGAAAGGAGAGCTTCCCAACTTAAAGCCATGTAACGAAAAATC	1560
Qy	1561	TAAATTAAGAGACTTGTCTTACTGACCAAGATATACAAAGCGTCCCTCACAAATA	1620
Dy	1561	TAAATTAAGAGACTTGTCTTACTGACCAAGATATACAAAGCGTCCCTCACAAATA	1620
Qy	1621	AAATTAAGCGTAAAGAGAGAGCTTAATAGAGCTTCACTCCAGAGATTTTATCAAGAAAG	1680
Dy	1621	AAATTAAGCGTAAAGAGAGAGCTTAATAGAGCTTCACTCCAGAGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAAGACTCTGTAATATATATCAAGAGAGCTTCTTCAAGAAAG	1740
Dy	1681	CAGATTTGGCAGTTCAAAAAGACTCTGTAATATATATCAAGAGAGCTTCTTCAAGAAAG	1740
Qy	1741	AGAAATGCTCAAGTGAATATATTAATTAATAGTGTATGAGATTAACCAAAAGGTGAT	1800
Dy	1741	AGAAATGCTCAAGTGAATATATTAATTAATAGTGTATGAGATTAACCAAAAGGTGAT	1800
Qy	1801	CTATTCAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTGGAATAAATCTGCTTCA	1860
Dy	1801	CTATTCAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTGGAATAAATCTGCTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTTAATGAAGCAGCTATTAAGCAATGTGAATCTCAATTAATATCC	1920
Dy	1861	AAACGAAAGCTGAACCTTAATGAAGCAGCTATTAAGCAATGTGAATCTCAATTAATATCC	1920
Qy	1921	ACAATTTCAAAAAGCACCCTTAATAAGATAGGCTGAGGAGGAGCTTCTACAGCATATTC	1980
Dy	1921	ACAATTTCAAAAAGCACCCTTAATAAGATAGGCTGAGGAGGAGCTTCTACAGCATATTC	1980
Qy	1981	ATGCGCTTGAAGTACTAGTCAATGATTAATCTTAAGCCCACTTAATGTATCTGAATTTGCAA	2040
Dy	1981	ATGCGCTTGAAGTACTAGTCAATGATTAATCTTAAGCCCACTTAATGTATCTGAATTTGCAA	2040
Qy	2041	TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAGTAAAGTAAAGTAAAGTAAAGT	2100
Dy	2041	TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAGTAAAGTAAAGTAAAGTAAAGT	2100
Qy	2101	GGCAGCAGAGAAACCTTACACTCATGAGAGGTAAAGAACTGTGCAACTGGAGCC	

Db	2341	CTAATAATGCTGAAGACCCCAAAAGATCTCATGTTAAAGTGGAGAAAGGGTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTGAAGCATATTTCAATTTGGTACTCGTACTGATTATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTGAAGCATATTTCAATTTGGTACTCGTACTGATTATGGCACTCAGG	2460
Qy	2461	AAAGATCTCGTTACTGTGAAGTTAGCACTCTAGGGAAGCCAAAACAGAACCAATAAT	2520
Db	2461	AAAGATCTCGTTACTGTGAAGTTAGCACTCTAGGGAAGCCAAAACAGAACCAATAAT	2520
Qy	2521	GTGGAGAGCAGGTGGCAGCAATTTGAAAACCCCAAGGAGCATTTTCATGATGGTTGTTCCAAAG	2580
Db	2521	GTGGAGAGCAGGTGGCAGCAATTTGAAAACCCCAAGGAGCATTTTCATGATGGTTGTTCCAAAG	2580
Qy	2581	ATAATAGAAAATGACACAGAAAGCGCTTTTAAGTATCCATGGGACATGAAAGTTAAACCAACATC	2640
Db	2581	ATAATAGAAAATGACACAGAAAGCGCTTTTAAGTATCCATGGGACATGAAAGTTAAACCAACATC	2640
Qy	2641	GGGAAACACACATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGATTTTGCAGAAATACAT	2700
Db	2641	GGGAAACACACATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGATTTTGCAGAAATACAT	2700
Qy	2701	TCAAGGTTTCAAAAGCCGCACTCATTTTGCTCTGTTTCAATCCAGAAATGCAAGAAAGG	2760
Db	2701	TCAAGGTTTCAAAAGCCGCACTCATTTTGCTCTGTTTCAATCCAGAAATGCAAGAAAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCACCTCTGGGTCTTTAAGGAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCCACCTCTGGGTCTTTAAGGAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATCACCTGCGAGCGCTTTCGTGTGGTGTGAGAAATATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACCTGCGAGCGCTTTCGTGTGGTGTGAGAAATATAGCCAGTTGATA	2940
Qy	2941	ATGCCAATGTAGATATCAAAAGAGCGCTAGGTTTGCTATCATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCCAATGTAGATATCAAAAGAGCGCTAGGTTTGCTATCATCTCAGTTCAAGAGCA	3000
Qy	3001	ACGAACTGACATCTATTCTCCAATTAACATGAGACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAACTGACATCTATTCTCCAATTAACATGAGACTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACCACTTTTCCCATCAATGACTTTTGTTTAAACTAAATGTAGAAAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAATGACTTTTGTTTAAACTAAATGTAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACCTTGAAGAACATTCATGATGCACTGAGAAAGAAATGGAAATGGAAACATGCCA	3180
Db	3121	AAAACCTTGAAGAACATTCATGATGCACTGAGAAAGAAATGGAAATGGAAACATGCCA	3180
Qy	3181	GTACAGTGAGCACAAATTAGCCCGTAATPAACATTAGAAAAATGTTTTTAAAGAGCCACT	3240
Db	3181	GTACAGTGAGCACAAATTAGCCCGTAATPAACATTAGAAAAATGTTTTTAAAGAGCCACT	3240
Qy	3241	CACACATATTTAATGAAGTGTGCCAGATGCTAATGACAGTGGGCTCCAGTATTAATGAA	3300
Db	3241	CACACATATTTAATGAAGTGTGCCAGATGCTAATGACAGTGGGCTCCAGTATTAATGAA	3300
Qy	3301	TAGGTCACAGATGAAGAAACATTCACAGACGAAGTGTGTAACAGAGGGCCAAAATATGA	3360
Db	3301	TAGGTCACAGATGAAGAAACATTCACAGACGAAGTGTGTAACAGAGGGCCAAAATATGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATTAACAAAGTCTTCCGGA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATTAACAAAGTCTTCCGGA	3420
Qy	3421	GTAATTTGTAAGCATCTCTGAAATATAAAAAGCAGAAATATGAGAGAGTGTGACACTGTTA	3480
Db	3421	GTAATTTGTAAGCATCTCTGAAATATAAAAAGCAGAAATATGAGAGAGTGTGACACTGTTA	3480

QY	3481	ATPACAGATTCTCTCCATATCTGATTTACAGATPACTTATAGAACGCCATATGGAGTACTC	3540
Db	3481	ATACAGATTCTCTCCATATCTGATTTACAGATPACTTATAGAACGCCATATGGAGTACTC	3540
QY	3541	ATGCATCTCAGGTTTGATCTTGAGACACCGATACCTGTTATGATGATGGTGAATPAAAG	3600
Db	3541	ATGCATCTCAGGTTTGATCTTGAGACACCGATGATGATGATGGTGAATPAAAG	3600
QY	3601	AAGATACTAGTTTGTGAAATGACATTPAAGAAAGTTCTGCTGTTTTAGCAAAACGC	3660
Db	3601	AAGATACTAGTTTGTGAAATGACATTPAAGAAAGTTCTGCTGTTTTAGCAAAACGC	3660
QY	3661	TCCGAAAAGGAGACTTACGAGAGAGTCGACCCCTTTCACCATACATTTGGTGCACG	3720
Db	3661	TCCGAAAAGGAGACTTACGAGAGAGTCGACCCCTTTCACCATACATTTGGTGCACG	3720
QY	3721	GTTACCCGAAGAGGGGCCAAGAAATATAGAGTCCTCAGAAAGAACTTATCTAGTGAAGTG	3780
Db	3721	GTTACCCGAAGAGGGGCCAAGAAATATAGAGTCCTCAGAAAGAACTTATCTAGTGAAGTG	3780
QY	3781	AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGACCGGTGCTACCGAGTGTGCTPAGAACACAGAGGGAATTTAT	3900
Db	3841	CTACTAGGCATAGACCGGTGCTACCGAGTGTGCTPAGAACACAGAGGGAATTTAT	3900
QY	3901	TATCATTTGAAATAGCTTTAAATGACTGCAGTAACCAAGGTAATATTTGGCAAAAGCATCTC	3960
Db	3901	TATCATTTGAAATAGCTTTAAATGACTGCAGTAACCAAGGTAATATTTGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACCTTAGAGSAGAAACAAATGTCGCTGATGTTTTCTTACAGTCA	4020
Db	3961	AGGAACATCACCTTAGAGSAGAAACAAATGTCGCTGATGTTTTCTTACAGTCA	4020
QY	4021	GTGATTTGGAAGACTTACATCGCAAAATACAAACACCCAGATCCTTCTTGATTGGTCTT	4080
Db	4021	GTGATTTGGAAGACTTACATCGCAAAATACAAACACCCAGATCCTTCTTGATTGGTCTT	4080
QY	4081	CCAAACAAATAGGCATCACTCTGAAAGCCAGGGAGTTGCTGAGTGCAAGAATTGG	4140
Db	4081	CCAAACAAATAGGCATCACTCTGAAAGCCAGGGAGTTGCTGAGTGCAAGAATTGG	4140
QY	4141	TTTCAGATGATGAAGAAGAGGAACGGGCTTGGAACAAATATATCAAGAAAGCAACCA	4200
Db	4141	TTTCAGATGATGAAGAAGAGGAACGGGCTTGGAACAAATATATCAAGAAAGCAACCA	4200
QY	4201	TGGAATCAAACCTTAGTGAAGACAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTGAGG	4260
Db	4201	TGGAATCAAACCTTAGTGAAGACAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTGAGG	4260
QY	4261	ACTGCTAAGGGCTTCTCTCAGAGTGAATTTAACCACTCAGAGAGGGATATACATGCG	4320
Db	4261	ACTGCTAAGGGCTTCTCTCAGAGTGAATTTAACCACTCAGAGAGGGATATACATGCG	4320
QY	4321	AACATTAACCTGATTAAGCCTCAGCAGGAATATGGCTTAACATAGACCTGTGTTAAGACGC	4380
Db	4321	AACATTAACCTGATTAAGCCTCAGCAGGAATATGGCTTAACATAGACCTGTGTTAAGACGC	4380
QY	4381	ATGGAGGCGACGCTTCTTAACAGCTACCCCTTCATTAAGTGAATCTTCTGCCCCTTGAGG	4440
Db	4381	ATGGAGGCGACGCTTCTTAACAGCTACCCCTTCATTAAGTGAATCTTCTGCCCCTTGAGG	4440
QY	4441	ACCTGCGAAATCCGAGCAACAGACATCAAGAAACAGATATTAATCTTCACGAAATA	4500
Db	4441	ACCTGCGAAATCCGAGCAACAGACATCAAGAAACAGATATTAATCTTCACGAAATA	4500
QY	4501	GTGAATTAACCTTAAGCCAGATATCCAGAAAGCCTTCTGCTGACAAAGTTTGAAGTGTCTG	4560
Db	4501	GTGAATTAACCTTAAGCCAGATATCCAGAAAGCCTTCTGCTGACAAAGTTTGAAGTGTCTG	4560





```
Db 181 TCTTGAAGTGTCCCATCTGCTGTGGAGTTGATCAAGAACTCTCTCCCAAAAGTGTGACC 240
Qy 241 ACATATTTTGGCAAAATTTTGGCATGCTGTAACCTTCTCCACAGAAAGAGGGCTTCACAGT 300
Db 241 ACATATTTTGGCAAAATTTTGGCATGCTGTAACCTTCTCCACAGAAAGAGGGCTTCACAGT 300
Qy 301 GTCCCTTTATGTAAGATATATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTACTC 360
Db 301 GTCCCTTTATGTAAGATATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTACTC 360
Qy 361 AACTGTGGAAGAGCTATTTGAAATCATTTGTGCTTTACAGTTGACAGAGTTGGAGT 420
Db 361 AACTGTGGAAGAGCTATTTGAAATCATTTGTGCTTTACAGTTGACAGAGTTGGAGT 420
Qy 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTGTAACATCTAAAGATG 480
Db 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTGTAACATCTAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGACTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGACTTCTACAGAGTG 540
Qy 541 AACCAGAAATCTCTCTCTGAGAGAAACAGCTCAGTGTCCAACTCTTAACCTGGAA 600
Db 541 AACCAGAAATCTCTCTCTGAGAGAAACAGCTCAGTGTCCAACTCTTAACCTGGAA 600
Qy 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACAACCTCAAAAGAGCTGTCTACATTTG 660
Db 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACAACCTCAAAAGAGCTGTCTACATTTG 660
Qy 661 AATTGGGATCTGATTTCTTCTGAAGTACCGTTTAATTAAGCAACTTATGCACTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTCTGAAGTACCGTTTAATTAAGCAACTTATGCACTGTGGAG 720
Qy 721 ATCAAGATTTGTACAAATCAACCCCTCAAGAGAACCGAGATGAATAGTATGATTTG 780
Db 721 ATCAAGATTTGTACAAATCAACCCCTCAAGAGAACCGAGATGAATAGTATGATTTG 780
Qy 781 CAAAAAGGCTGCTTGTGAATTTCTGAGAGCGATTAACAATTAAGCAACTTATGCACTGTGGAG 840
Db 781 CAAAAAGGCTGCTTGTGAATTTCTGAGAGCGATTAACAATTAAGCAACTTATGCACTGTGGAG 840
Qy 841 CCAGTAATTAATGATTTGAAACACACTGAAAGCGTGTGAGAGGCAATCCAGAAAAGT 900
Db 841 CCAGTAATTAATGATTTGAAACACACTGAAAGCGTGTGAGAGGCAATCCAGAAAAGT 900
Qy 901 ATCAGGAGTGTGTTGTTCAAACTGATGAGAGCGATGAGGCAATGCTCATGCA 960
Db 901 ATCAGGAGTGTGTTGTTCAAACTGATGAGAGCGATGAGGCAATGCTCATGCA 960
Qy 961 GCTCATTAACAGCATGAGAAACAGAGTTTATTAATTAAGAGAGAGATGAATGATGAAA 1020
Db 961 GCTCATTAACAGCATGAGAAACAGAGTTTATTAATTAAGAGAGAGATGAATGATGAAA 1020
Qy 1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGCTTGTGCAAGAGGCCAATTAACAGAT 1080
Db 1021 AGGCTGAATTTCTGTAATTAAGCAACAGCTGCTTGTGCAAGAGGCCAATTAACAGAT 1080
Qy 1081 GGGCTGAGAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCAGCAAAAAGGGTGG 1140
Db 1081 GGGCTGAGAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCAGCAAAAAGGGTGG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAGAACTGCCATCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAGAACTGCCATCT 1200
Qy 1201 CAGAGAAATCTAGAGATCTGAAAGATGTTCTTGATTAACCTTAATTAAGCAGATTCAGA 1260
Db 1201 CAGAGAAATCTAGAGATCTGAAAGATGTTCTTGATTAACCTTAATTAAGCAGATTCAGA 1260
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGTGATGTTCTGATACATGATG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGATGATGTTCTGATACATGATG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGATGATGTTCTGATACATGATG 1320
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGATTTGAGAGTCTTAATAGSTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGATTTGAGAGTCTTAATAGSTAGATG 1380
Qy 1381 AATATTCGTTCTTCAGAGAAATTAAGCTTAAGGCGAGAGATCCATAGAGCTTTAA 1440
Db 1381 AATATTCGTTCTTCAGAGAAATTAAGCTTAAGGCGAGAGATCCATAGAGCTTTAA 1440
Qy 1441 TATGTAAAGGAAAGAGTGTACTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT 1500
Db 1441 TATGTAAAGGAAAGAGTGTACTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT 1500
Qy 1501 TTGGGAAAACCTTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAAGTAAATC 1560
Db 1501 TTGGGAAAACCTTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAAGTAAATC 1560
Qy 1561 TAAATTAAGAGCATTTGTTCTGAGGCAAGATTAATCAAGAGAGGCTCCCAATA 1620
Db 1561 TAAATTAAGAGCATTTGTTCTGAGGCAAGATTAATCAAGAGAGGCTCCCAATA 1620
Qy 1621 AATTAAGCCGTAAGAGAGAGACTACATCAGGCTTCAATCTGAGAGATTTTCAAGAAAG 1680
Db 1621 AATTAAGCCGTAAGAGAGAGACTACATCAGGCTTCAATCTGAGAGATTTTCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAAAAAGACTCTGTAATGATTAATCAGGAGACTTAACCAACGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTGTAATGATTAATCAGGAGACTTAACCAACGAGC 1740
Qy 1741 AGAATGGCAAGTATGAATTTTCTAATTAAGTGTGATGATGAATTAAGAAAGTGT 1800
Db 1741 AGAATGGCAAGTATGAATTTTCTAATTAAGTGTGATGATGAATTAAGAAAGTGT 1800
Qy 1801 CTATTGCAATGAGAAAAATCTTAACCAATGAGATCACTGAAAGAAATCTGCTTCA 1860
Db 1801 CTATTGCAATGAGAAAAATCTTAACCAATGAGATCACTGAAAGAAATCTGCTTCA 1860
Qy 1861 AAACGAAAGCTGAACCTTAAGAGAGAGATTAAGCAATTAAGAACTGAAATTAATCC 1920
Db 1861 AAACGAAAGCTGAACCTTAAGAGAGAGATTAAGCAATTAAGAACTGAAATTAATCC 1920
Qy 1921 ACAATTTCAAAAGCACCTTAAGAAATAGGCTGAGAGAGAGTCTTCAACGAGATATTC 1980
Db 1921 ACAATTTCAAAAGCACCTTAAGAAATAGGCTGAGAGAGAGTCTTCAACGAGATATTC 1980
Qy 1981 ATGGGCTGAACCTAGTGTGCTAGAAATCTAAGCCACCTAATTTGTAAGTGA 2040
Db 1981 ATGGGCTGAACCTAGTGTGCTAGAAATCTAAGCCACCTAATTTGTAAGTGA 2040
Qy 2041 TTGATAGTGTGTTCTAGAGAGTGAAGATTAAGAAAAAGTAAACCAATTAAGCAGTCA 2100
Db 2041 TTGATAGTGTGTTCTAGAGAGTGAAGATTAAGAAAAAGTAAACCAATTAAGCAGTCA 2100
Qy 2101 GGCACAGCAGAAACCTTAACACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
Db 2101 GGCACAGCAGAAACCTTAACACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
Qy 2161 GTAAACAAGCCAAATGAAGACAGAGTAAAGACATGACAGAGACTTTCCACAGAGTGA 2220
Db 2161 GTAAACAAGCCAAATGAAGACAGAGTAAAGACATGACAGAGACTTTCCACAGAGTGA 2220
Qy 2221 AGTTAACAATGACACTGTGTTCTTTACTAAGTGTCAAAATTAAGCAGTGAATTAAGAT 2280
Db 2221 AGTTAACAATGACACTGTGTTCTTTACTAAGTGTCAAAATTAAGCAGTGAATTAAGAT 2280
Qy 2281 TTGTCAATCTAGGCTTCCAAAGAGAGAGAAAGAACTTGAAGACGTTAAAGTGT 2340
Db 2281 TTGTCAATCTAGGCTTCCAAAGAGAGAGAGAAAGAACTTGAAGACGTTAAAGTGT 2340
Qy 2341 CTAATTAATGCTGAAGAGCCCAAGAGATCTCATGTTAAGTGGAGAAAGGTTTGGAAACTG 2400
Db 2341 CTAATTAATGCTGAAGAGCCCAAGAGATCTCATGTTAAGTGGAGAAAGGTTTGGAAACTG 2400
```





D	b	181	TCCTAGAGCTGCCATCTGTCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTACC	240
Q	y	241	ACATATTTTGGAAATTTTGCATGCTGAAACTTCTCAACGAGAAAGGGCCTTCACAGT	300
D	b	241	ACATATTTTGGAAATTTTGCATGCTGAAACTTCTCAACGAGAAAGGGCCTTCACAGT	300
Q	y	301	GTCCTTATGTAGAAATGATATACCCAAAGAGCCCTACAGAAAGTACAGATTTAGTC	360
D	b	301	GTCCTTATGTAGAAATGATATACCCAAAGAGCCCTACAGAAAGTACAGATTTAGTC	360
Q	y	361	AACCTGTGAAGAGCTATTTGAATCATTTGTGCTTTTCAGTTTGACATGACAGGTTGGAGT	420
D	b	361	AACCTGTGAAGAGCTATTTGAATCATTTGTGCTTTTCAGTTTGACATGACAGGTTGGAGT	420
Q	y	421	ATGCAAAACAGCTATTAATTTTGGCAAAAAGAAATTAACCTCTCTGACATCTTAAGAGATG	480
D	b	421	ATGCAAAACAGCTATTAATTTTGGCAAAAAGAAATTAACCTCTCTGACATCTTAAGAGATG	480
Q	y	481	AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG	540
D	b	481	AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG	540
Q	y	541	AACCCGAAATCCTCTCTTGCGAGAAACCAAGTCTGAGTCCAGCTCTTAACCTTGGAA	600
D	b	541	AACCCGAAATCCTCTCTTGCGAGAAACCAAGTCTGAGTCCAGCTCTTAACCTTGGAA	600
Q	y	601	CTGTGAGAACTCTGAGCAAAAGCAGCGGATTAACAACCTCAAAAAGAGTCTGTCTACATTTG	660
D	b	601	CTGTGAGAACTCTGAGCAAAAGCAGCGGATTAACAACCTCAAAAAGAGTCTGTCTACATTTG	660
Q	y	661	AATGGGATCTGATTTCTCTGAAAGTACCGTTTAATTAAGCAACTTATTCAGTGTGGAG	720
D	b	661	AATGGGATCTGATTTCTCTGAAAGTACCGTTTAATTAAGCAACTTATTCAGTGTGGAG	720
Q	y	721	ATCAGAATTTGTACAAATCAACCCCTCAAGGAACCGGATGAATTCAGTTGGATTCTG	780
D	b	721	ATCAGAATTTGTACAAATCAACCCCTCAAGGAACCGGATGAATTCAGTTGGATTCTG	780
Q	y	781	CAAAAAGGCTGCTTGTGTAATTTTCTGAGAGGATGTAAACAAATCTGAAATCATCAAC	840
D	b	781	CAAAAAGGCTGCTTGTGTAATTTTCTGAGAGGATGTAAACAAATCTGAAATCATCAAC	840
Q	y	841	CCAGTAATTAATGATTTGACACCACTGAGAAAGCCGTGACGTGAGAGCATCCAGAAAGT	900
D	b	841	CCAGTAATTAATGATTTGACACCACTGAGAAAGCCGTGACGTGAGAGCATCCAGAAAGT	900
Q	y	901	ATCAGGATAGTCTGTTCAAACTGATGTGAGCCATGTGGCAACAATACTCATGCCA	960
D	b	901	ATCAGGATAGTCTGTTCAAACTGATGTGAGCCATGTGGCAACAATACTCATGCCA	960
Q	y	961	GCTCATTACAGATGAGAACAGAGCTTATTACTACTAAAGACAGAAATGATGAGAA	1020
D	b	961	GCTCATTACAGATGAGAACAGAGCTTATTACTACTAAAGACAGAAATGATGAGAA	1020
Q	y	1021	AGGCTGAATTTCTTAATTAAGCAAAAGCAGCTGCTTGAAGGAGGCCAACAATAACAAT	1080
D	b	1021	AGGCTGAATTTCTTAATTAAGCAAAAGCAGCTGCTTGAAGGAGGCCAACAATAACAAT	1080
Q	y	1081	GGGCTGGAAGTAAGGAAACATGTAATAGGCGGACTCCAGCACAGAAAAAAGGTAG	1140
D	b	1081	GGGCTGGAAGTAAGGAAACATGTAATAGGCGGACTCCAGCACAGAAAAAAGGTAG	1140
Q	y	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATTAAGCAGAAACTGCCATCT	1200
D	b	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATTAAGCAGAAACTGCCATCT	1200
Q	y	1201	CAGGAATCCAGAGATACTGAAGATGTTCTCTGATTAACACTAAATAGCAGACTTCGA	1260
D	b	1201	CAGGAATCCAGAGATACTGAAGATGTTCTCTGATTAACACTAAATAGCAGACTTCGA	1260
Q	y	1261	AAGTTAATGAGTGGTTTCCAGAAAGTGAAGTGAAGTTAGTTCTGATGACTACATGATG	1320
D	b	1261	AAGTTAATGAGTGGTTTCCAGAAAGTGAAGTGAAGTTAGTTCTGATGACTACATGATG	1320

---

Q	y	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATTTGAGCGTTCTTAATGAGTAGATG	1380
D	b	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATTTGAGCGTTCTTAATGAGTAGATG	1380
Q	y	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGAATCCTCATGAGGCTTTAA	1440
D	b	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGAATCCTCATGAGGCTTTAA	1440
Q	y	1441	TATGTAAAGTGAAGAGTACTACTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
D	b	1441	TATGTAAAGTGAAGAGTACTACTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
Q	y	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCATGTAACGAAATTC	1560
D	b	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCATGTAACGAAATTC	1560
Q	y	1561	TAAATATGAGACATTTGTTACTAGCCACAGATTAATACAGAGCGTCCCTCACAATAA	1620
D	b	1561	TAAATATGAGACATTTGTTACTAGCCACAGATTAATACAGAGCGTCCCTCACAATAA	1620
Q	y	1621	AATTAAGCTTAAGAGAGACCTACATCAGGCTTCATCCTGAGAGATTTATCAAGAAATG	1680
D	b	1621	AATTAAGCTTAAGAGAGACCTACATCAGGCTTCATCCTGAGAGATTTATCAAGAAATG	1680
Q	y	1681	CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGAATTAACCAACGAGAC	1740
D	b	1681	CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGAATTAACCAACGAGAC	1740
Q	y	1741	AGAATGCTCAAGTATGAATTTACTAATAGTGTCTATGAGATTAACCAAGAGTGATT	1800
D	b	1741	AGAATGCTCAAGTATGAATTTACTAATAGTGTCTATGAGATTAACCAAGAGTGATT	1800
Q	y	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGATACATCGAAAAAGAAATTCGTTTCA	1860
D	b	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGATACATCGAAAAAGAAATTCGTTTCA	1860
Q	y	1861	AAAGAAAAGCTGAACCTATTAAGCAGAGTATTAAGCAATATGAGAACTGAATTAATTC	1920
D	b	1861	AAAGAAAAGCTGAACCTATTAAGCAGAGTATTAAGCAATATGAGAACTGAATTAATTC	1920
Q	y	1921	ACAATTAAGAAAGCACTTAAGAAATAGGCTGAGAGAGAGTCTTACACGACATATTC	1980
D	b	1921	ACAATTAAGAAAGCACTTAAGAAATAGGCTGAGAGAGAGTCTTACACGACATATTC	1980
Q	y	1981	ATGCGCTTGAACCTAGTGTGATGATGAATCTAAGCCACCTAATTTAGTGAATTCGAAA	2040
D	b	1981	ATGCGCTTGAACCTAGTGTGATGATGAATCTAAGCCACCTAATTTAGTGAATTCGAAA	2040
Q	y	2041	TTGATAGTGTCTTAGCAGTGAAGAGATTAAGAAAAAAGTCAACCAAAATCCAGTCA	2100
D	b	2041	TTGATAGTGTCTTAGCAGTGAAGAGATTAAGAAAAAAGTCAACCAAAATCCAGTCA	2100
Q	y	2101	GGCAGACAGAAACCTCAACTCATGGAAGTAAAGAACTGCACTGAGGCCAAGAAGA	2160
D	b	2101	GGCAGACAGAAACCTCAACTCATGGAAGTAAAGAACTGCACTGAGGCCAAGAAGA	2160
Q	y	2161	GTAACAAGCCAAATGAGACACAAATTAAGAGATGACAGCATTTTCCAGAGCTGA	2220
D	b	2161	GTAACAAGCCAAATGAGACACAAATTAAGAGATGACAGCATTTTCCAGAGCTGA	2220
Q	y	2221	AGTTAACAATAATGACACCTGGTCTTTTACTAAGTGTCAATTAACAGTGAACCTTAAGAAAT	2280
D	b	2221	AGTTAACAATAATGACACCTGGTCTTTTACTAAGTGTCAATTAACAGTGAACCTTAAGAAAT	2280
Q	y	2281	TTGTCAATCCTAGCCTTCCAGAGAGAGAAAAAGAAAGAACTAGAAAGTTAAAGTGT	2340
D	b	2281	TTGTCAATCCTAGCCTTCCAGAGAGAGAAAAAGAAAGAACTAGAAAGTTAAAGTGT	2340
Q	y	2341	CTAATTAATGCTGAAGAACCCCAAGAAATCTCATGTTAAGTGAGAGAAAGGTTTTCAGAACTG	2400
D	b	2341	CTAATTAATGCTGAAGAACCCCAAGAAATCTCATGTTAAGTGAGAGAAAGGTTTTCAGAACTG	2400



```

Db 4561 CAGATAGTCTACCAAGTAAATAAGAACAGAGTGGAAAGTCAATCCCTTTAAAT 4620
QY 4621 GCCCATATTAGATGATAGTGTGTACATGACAGAGTGTCTGGAGTCTTCAGAAATAGA 4680
    |||||||
Db 4621 GCCCATATTAGATGATAGTGTGTACATGACAGAGTGTCTGGAGTCTTCAGAAATAGA 4680
QY 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTTGTTGATGTGAGAGACACAGCTGGAG 4740
    |||||||
Db 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTTGTTGATGTGAGAGACACAGCTGGAG 4740
QY 4741 AGTCTGGGCCACAGATTTGAGCGGAACATCTTACTTGGCAAGGAGAGTCTAGAGGGA 4800
    |||||||
Db 4741 AGTCTGGGCCACAGATTTGAGCGGAACATCTTACTTGGCAAGGAGAGTCTAGAGGGA 4800
QY 4741 AGTCTGGGCCACAGATTTGAGCGGAACATCTTACTTGGCAAGGAGAGTCTAGAGGGA 4800
    |||||||
QY 4801 CCCCTTACTGGAATCTGGAATTCAGCCCTTCTCTGATGACCCCTGAATCTGATCTTCTG 4860
    |||||||
Db 4801 CCCCTTACTGGAATCTGGAATTCAGCCCTTCTCTGATGACCCCTGAATCTGATCTTCTG 4860
QY 4861 AAGACAGAGCCCGAGAGTCTGTGTGGACATACATCTTCAACCTTGCATTGA 4920
    |||||||
Db 4861 AAGACAGAGCCCGAGAGTCTGTGTGGACATACATCTTCAACCTTGCATTGA 4920
QY 4921 AAGTCCCAATTAAGTTGTCAGAAATCTGCCAGAGTCCAGCTGCTGCTCATCTACTG 4980
    |||||||
Db 4921 AAGTCCCAATTAAGTTGTCAGAAATCTGCCAGAGTCCAGCTGCTGCTCATCTACTG 4980
QY 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAGAAATTTGACAG 5040
    |||||||
Db 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAGAAATTTGACAG 5040
QY 5041 CTTCACAGAGAGGCTCAACAAAGAAATGTCATGCTGTGCTGCTGACCCGACAGAG 5100
    |||||||
Db 5041 CTTCACAGAGAGGCTCAACAAAGAAATGTCATGCTGTGCTGCTGACCCGACAGAG 5100
QY 5101 AATTATGCTGCTGTACAAAGTTGGCAGAAACACACATCACTTAACTAATTAATTA 5160
    |||||||
Db 5101 AATTATGCTGCTGTACAAAGTTGGCAGAAACACACATCACTTAACTAATTAATTA 5160
QY 5161 CTGAAGAGTCTACTCATGTTTATGAAAACAGATGCTGAGTTTGTGTGACGAGAC 5220
    |||||||
Db 5161 CTGAAGAGTCTACTCATGTTTATGAAAACAGATGCTGAGTTTGTGTGACGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATTCGGGAGGAGAAATGGGTAGTAACTTCTGGGAGACC 5280
    |||||||
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAGAAATGGGTAGTAACTTCTGGGAGACC 5280
QY 5281 AGCTATTTAAAGAAAGAAATGCTGTAATGAGCATGATTTTGAATCAGAGAGATGTGG 5340
    |||||||
Db 5281 AGCTATTTAAAGAAAGAAATGCTGTAATGAGCATGATTTTGAATCAGAGAGATGTGG 5340
QY 5341 TCATGGAAGAAACCCAGAGGTCCTCAAGGACAGAGAAATCCGAGACAGAAAGATCT 5400
    |||||||
Db 5341 TCATGGAAGAAACCCAGAGGTCCTCAAGGACAGAGAAATCCGAGACAGAAAGATCT 5400
QY 5401 TCAGGGGGCTAGGAATCTGTTGATGGGCTTCAACCAATATGGCCACAGATCAACG 5460
    |||||||
Db 5401 TCAGGGGGCTAGGAATCTGTTGATGGGCTTCAACCAATATGGCCACAGATCAACG 5460
QY 5461 AATGATGATGACAGCTGTGTGCTTCTGTGTGTAAGAGACTTTCATTCACCTTGG 5520
    |||||||
Db 5461 AATGATGATGACAGCTGTGTGCTTCTGTGTGTAAGAGACTTTCATTCACCTTGG 5520
QY 5521 GCACAGTGTCCACCAATTTGTTGTGACGACAGATGCTTGGACAGAGACAAATGGCT 5580
    |||||||
Db 5521 GCACAGTGTCCACCAATTTGTTGTGACGACAGATGCTTGGACAGAGACAAATGGCT 5580
QY 5581 TCATGGAATTTGGCAGATGTGTGAGGACACTGTGTGAGACCGGAGAGGTTTGGACA 5640
    |||||||
Db 5581 TCATGGAATTTGGCAGATGTGTGAGGACACTGTGTGAGACCGGAGAGGTTTGGACA 5640
QY 5641 GTGTAGAGTCTTACAGTGCAGAGAGTGCAGACCTTACTATATACCCAGATGCCCCACA 5700
    |||||||
Db 5641 GTGTAGAGTCTTACAGTGCAGAGAGTGCAGACCTTACTATATACCCAGATGCCCCACA 5700

```

```

QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 6
V46459
ID V46459 standard; cDNA; 5711 BP.
AC V46459;
DT 18-NOV-1998 (first entry)
DE Human BRCA1 omi2 polymorphism #2 cDNA.
KW BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..5711
FT FT /*tag= a
FT FT /product= "BRCA1 omi2 protein"
FT FT variation 2430
FT FT /*tag= b
FT FT /note= "This polymorphic variation can be a T or C
FT FT nucleotide"
FN US5750400-A.
PD 12-MAY-1998.
PR 12-FEB-1997; 798691.
PR 12-FEB-1996; US-598591.
PR 12-FEB-1997; US-798691.
PA (ONCO-) ONCOMED INC.
PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,
PI Schelter DB, Zeng B;
DR WPI: 98-296774/26.
PT BRCA1 omi gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
PS Claim 2e: Page -: 54pp; English.
CC This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi2 gene in which a polymorphic variation occurs at
CC nucleotide 2430. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi2 gene represented in V46449.
SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T;

Query Match 100.0%; Score 5710.6; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTCGTGAAGACTTCTGTGACCCCGACAGAGCTGTGGGGTTCTCAGATACTGGCC 60
    |||||||
Db 1 AGCTCGTGAAGACTTCTGTGACCCCGACAGAGCTGTGGGGTTCTCAGATACTGGCC 60
QY 61 CTTGCGCTCAGAGAGGCTTCAACCTTCTGTGCTGTGTAAGATTGTAACAGAAAGAAA 120
    |||||||
Db 61 CTTGCGCTCAGAGAGGCTTCAACCTTCTGTGCTGTGTAAGATTGTAACAGAAAGAAA 120
QY 121 TGAATTAATGCTGCTTCTGCGGTTGAGAGAAATACAAATGCTATTAATGCTATGCAAAAA 180
    |||||||
Db 121 TGAATTAATGCTGCTTCTGCGGTTGAGAGAAATACAAATGCTATTAATGCTATGCAAAAA 180
QY 121 TGAATTAATGCTGCTTCTGCGGTTGAGAGAAATACAAATGCTATTAATGCTATGCAAAAA 180
    |||||||
Db 121 TGAATTAATGCTGCTTCTGCGGTTGAGAGAAATACAAATGCTATTAATGCTATGCAAAAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGTGAGTGTGATCAAGAGAACTGTCTCCAAAGTGTGACC 240
    |||||||
Db 181 TCTTAGAGTGTCCCATCTGTCTGTGAGTGTGATCAAGAGAACTGTCTCCAAAGTGTGACC 240

```







```
|||||
Db 2401 AAGAGCTCTAGAGAGTAGAGATTTTCATGTGACTGTACTGATTAGGCACTGAG 2460
Oy 2461 AAGATATCTGTTACTGGAAGTAGCACTTAGGGAAGCAAAACAGAACCAATTAAT 2520
|||
Db 2461 AAGATATCTGTTACTGGAAGTAGCACTTAGGGAAGCAAAACAGAACCAATTAAT 2520
Oy 2521 GTGTGAGTCAGTGTGCAGCATTTTGAAAAACCCCAAGGAGCTAATTCATGTTTCCAAAG 2580
|||
Db 2521 GTGTGAGTCAGTGTGCAGCATTTTGAAAAACCCCAAGGAGCTAATTCATGTTTCCAAAG 2580
Oy 2581 ATAAATGAATGACAGAGAGGCTTAAATATCATTTGGAGACATGAAGTTAACACAGTC 2640
|||
Db 2581 ATAAATGAATGACAGAGAGGCTTAAATATCATTTGGAGACATGAAGTTAACACAGTC 2640
Oy 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACTGATGCTCAGTATTTTCAGAAATCAT 2700
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACTGATGCTCAGTATTTTCAGAAATCAT 2700
Oy 2701 TCAAGTTTCAAAAGCCCGCAGTCAATTTGCTGTGTTTCAAAATCCAGAAATGCAGAGAGG 2760
|||
Db 2701 TCAAGTTTCAAAAGCCCGCAGTCAATTTGCTGTGTTTCAAAATCCAGAAATGCAGAGAGG 2760
Oy 2761 AATGTGCAACATTTCTGCCCCACTGTGGGTCCTTAAAGAAACAAGTCCAAAGTCACTT 2820
|||
Db 2761 AATGTGCAACATTTCTGCCCCACTGTGGGTCCTTAAAGAAACAAGTCCAAAGTCACTT 2820
Oy 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATGAGTCAATATCAAGCCTGTAC 2880
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATGAGTCAATATCAAGCCTGTAC 2880
Oy 2881 AGACAGTTAATATCACTGCAGGCTTCCCTGTGTTGGTGCAGAAAGATAGCCAGTTGATA 2940
Db 2881 AGACAGTTAATATCACTGCAGGCTTCCCTGTGTTGGTGCAGAAAGATAGCCAGTTGATA 2940
Oy 2941 ATGCCAAATGTATCAAGAGAGGCTAGGTTTGTATCATCTCAGTTAGAGGCA 3000
|||
Db 2941 ATGCCAAATGTATCAAGAGAGGCTAGGTTTGTATCATCTCAGTTAGAGGCA 3000
Oy 3001 ACGAAACCTGACTCATTTACTCCAAATTAACATGAGACTTTTACAAAACCATATCGTATAC 3060
Db 3001 ACGAAACCTGACTCATTTACTCCAAATTAACATGAGACTTTTACAAAACCATATCGTATAC 3060
Oy 3061 CACCACTTTTCCCATCACTGATTTGTTAAATGTAAGAAAACTCTCTGAGG 3120
|||
Db 3061 CACCACTTTTCCCATCACTGATTTGTTAAATGTAAGAAAACTCTCTGAGG 3120
Oy 3121 AAAACCTTTGAGGAACATTCATGTCACTGAAAGAGAAATGGAAATGAGAACATTCCAA 3180
Db 3121 AAAACCTTTGAGGAACATTCATGTCACTGAAAGAGAAATGGAAATGAGAACATTCCAA 3180
Oy 3181 GTACAGTGAACAATTAACCGCTAATTAACATTAAGAAAAATGTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTGAACAATTAACCGCTAATTAACATTAAGAAAAATGTTTAAAGAGCCAGCT 3240
Oy 3241 CAAGCAATATTAATGAAGTAGTTCACGACTAATGAAGTGGGCTCCAGATTAATGAAA 3300
Db 3241 CAAGCAATATTAATGAAGTAGTTCACGACTAATGAAGTGGGCTCCAGATTAATGAAA 3300
Oy 3301 TAGGTTCCAGTATGAAAAATTCAGAGCAAGAACTAGTGAAGAACAGAGGCCAAAATTGA 3360
Db 3301 TAGGTTCCAGTATGAAAAATTCAGAGCAAGAACTAGTGAAGAACAGAGGCCAAAATTGA 3360
Oy 3361 ATGCTATGCTTAGATTAGGAGGTTTGGCAACTGAGGTCATTAACAAGTCTTCTGGA 3420
Db 3361 ATGCTATGCTTAGATTAGGAGGTTTGGCAACTGAGGTCATTAACAAGTCTTCTGGA 3420
Oy 3421 GTAATGTAAAGCATCTGAATTAATAAAGCAAGAAATATGAAGAGTAGTTTCAGACGTGA 3480
Db 3421 GTAATGTAAAGCATCTGAATTAATAAAGCAAGAAATATGAAGAGTAGTTTCAGACGTGA 3480
Oy 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAACCTTAGAACAGCTATGGGAAGTAGTC 3540
|||
```

```
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCTTATGGAGTAGTC 3540
Oy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTAAATTAAG 3600
|||
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTAAATTAAG 3600
Oy 3601 AAGATACATGTTTGTCTGAAAATGACATTAAGAGAAAGTTCTCTGTTTTCAGAAAACG 3660
|||
Db 3601 AAGATACATGTTTGTCTGAAAATGACATTAAGAGAAAGTTCTCTGTTTTCAGAAAACG 3660
Oy 3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGCCCTTTCACCATACATTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGCCCTTTCACCATACATTTGGCTCAGG 3720
Oy 3721 GTTACCGAAGAGGAGGCAAGAAATTAAGTCTCTCAGAAAGAACTTATCTAGTAGATG 3780
Db 3721 GTTACCGAAGAGGAGGCAAGAAATTAAGTCTCTCAGAAAGAACTTATCTAGTAGATG 3780
Oy 3781 AAGAGCTTCCCTGCTTCAACACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCAACACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Oy 3841 CTACTAGCATATGACACCGTTGCTACCGAGTGTGCTTAAGAACACAGAGAGAAATTAAT 3900
Db 3841 CTACTAGCATATGACACCGTTGCTACCGAGTGTGCTTAAGAACACAGAGAGAAATTAAT 3900
Oy 3901 TATCATTTGAAGATATACCTTAAATGAATGACATGACATTAATTTGGCAAGGATCTC 3960
Db 3901 TATCATTTGAAGATATACCTTAAATGAATGACATGACATTAATTTGGCAAGGATCTC 3960
Oy 3961 AGGAACATCACTTATGAGGAAACAAAATGTTGCTGATAGCTGTTTCTTCAACAGTGA 4020
Db 3961 AGGAACATCACTTATGAGGAAACAAAATGTTGCTGATAGCTGTTTCTTCAACAGTGA 4020
Oy 4021 GTGAATTTGAAGACTGATGCAAAATACAAACACCCAGATCTTCTTGAATGGTCTT 4080
Db 4021 GTGAATTTGAAGACTGATGCAAAATACAAACACCCAGATCTTCTTGAATGGTCTT 4080
Oy 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCCAGAGAGTTGGTCTGAGTGAACAAGAAATGG 4140
Db 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCCAGAGAGTTGGTCTGAGTGAACAAGAAATGG 4140
Oy 4141 TTTCAATATTAAGAAAGAGAGAGAGGCTTGGAGAAATTAATCAAGAAAGCA 4200
Db 4141 TTTCAATATTAAGAAAGAGAGAGAGGCTTGGAGAAATTAATCAAGAAAGCA 4200
Oy 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTTGAGAGTGAAGAAACAGGCTCTGAG 4260
Db 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTTGAGAGTGAAGAAACAGGCTCTGAG 4260
Oy 4261 ACTGCTCAGGAGCTATCTCTCAGAGTGAACATTTTAACACTCAGCAGAGAGATACATGC 4320
Db 4261 ACTGCTCAGGAGCTATCTCTCAGAGTGAACATTTTAACACTCAGCAGAGAGATACATGC 4320
Oy 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGCGTGAACCTAGAAAGCTGTTTAACAACG 4380
Db 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGCGTGAACCTAGAAAGCTGTTTAACAACG 4380
Oy 4381 ATGGAGCAGAGCTTCTTAACAGACTACCTTCATCATTAAGAGACTCTTCTGAGG 4440
Db 4381 ATGGAGCAGAGCTTCTTAACAGACTACCTTCATCATTAAGAGACTCTTCTGAGG 4440
Oy 4441 ACCTCGAAAATCCAGAAACAAAGCAGATCAGAAAAAGCAGTATTAACCTCAGAAAAAGTA 4500
Db 4441 ACCTCGAAAATCCAGAAACAAAGCAGATCAGAAAAAGCAGTATTAACCTCAGAAAAAGTA 4500
Oy 4501 GTGAATTAACCTTAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAGATTTGAGGAGTGTG 4560
Db 4501 GTGAATTAACCTTAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAGATTTGAGGAGTGTG 4560
Oy 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Db 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620
```

QY	4621	GCCCATATATAGATAGTGGTGTATCATGCACAGTGGCTGTGGAGTCTTCAGATTACA	4680
Db	4621	GCCCATATATAGTATAGTGGTGTATCATGCACAGTGGCTGTGGAGTCTTCAGATTAGA	4680
QY	4681	ACTACCCATCTCAAGAGAGACTCATTAAAGTGTGTATGTGAGGAGCAACAGCTGAAG	4740
Db	4681	ACTACCCATCTCAAGAGAGAGACTCATTAAAGTGTGTATGTGAGGAGCAACAGCTGAAAG	4740
QY	4741	AGCTGGGGCCACAGATTGAGCGGAAACATTACTTGCAGAGGCAAGATCTGAGGGAA	4800
Db	4741	AGCTGGGGCCACAGATTGAGCGGAAACATTACTTGCAGAGGCAAGATCTGAGGGAA	4800
QY	4801	CCCCCTACCTGGATCTGSAATCAGGCTCTTCTCTGATACCCCTGAATCTGATCCCTTCTG	4860
Db	4801	CCCCCTACCTGGATCTGSAATCAGGCTCTTCTCTGATACCCCTGAATCTGATCCCTTCTG	4860
QY	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTTGGCAACATACCATTCTTCAACCTCTGCATTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTTGGCAACATACCATTCTTCAACCTCTGCATTGA	4920
QY	4921	AAGTCCCCCAATTGAAAGTGGCAGATCTGCCAGAGTCCAGCTCTGTCATCTACTACTG	4980
Db	4921	AAGTCCCCCAATTGAAAGTGGCAGATCTGCCAGAGTCCAGCTCTGTCATCTACTACTG	4980
QY	4981	ATATCTGTGGGTATTAATGCATGGAAGAAAGTGTGAGCGGAGAGACCGAATTGACAG	5040
Db	4981	ATATCTGTGGGTATTAATGCATGGAAGAAAGTGTGAGCGGAGAGACCGAATTGACAG	5040
QY	5041	CTTCAACAGAAAGGTCACAAACAAAGAAATGCCATGGTGGTGTCTGGCTGACCCCAAGAG	5100
Db	5041	CTTCAACAGAAAGGTCACAAACAAAGAAATGCCATGGTGGTGTCTGGCTGACCCCAAGAG	5100
QY	5101	AATTATGCTCGTGTACAAAGTTGGCCAGAAAACACACATCACTTAACTAATCTAATTA	5160
Db	5101	AATTATGCTCGTGTACAAAGTTGGCCAGAAAACACACATCACTTAACTAATCTAATTA	5160
QY	5161	CTGAAAGAGACTACTCATGTGTTATGAAAAACAGATGCTGAGTTGTGTGTGACAGGACAC	5220
Db	5161	CTGAAAGAGACTACTCATGTGTTATGAAAAACAGATGCTGAGTTGTGTGTGACAGGACAC	5220
QY	5221	TGAAATTTTTCTTNGAATGCGCGGAGGAAATGGGTATTGATCTGTCGTTCTGCGTGACGACAC	5280
Db	5221	TGAAATTTTTCTTNGAATGCGCGGAGGAAATGGGTATTGATCTGTCGTTCTGCGTGACAC	5280
QY	5281	AGTCTATTAAAGAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG	5340
QY	5341	TCATATGGAAGAAACCCAAAGTCCAAAGCCAGAGCAAGAAATCCCAAGGACAGAAAGATCT	5400
Db	5341	TCATATGGAAGAAACCCAAAGTCCAAAGCCAGAGCAAGAAATCCCAAGGACAGAAAGATCT	5400
QY	5401	TCAAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCCACAACTGCCCCACAGATCAACTGG	5460
Db	5401	TCAAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCCACAACTGCCCCACAGATCAACTGG	5460
QY	5461	AATGATGCTACAGCTGTGTGTGCTTCTGTGTGTAAGGAGAGCTTTCATCATTCACCTCTTG	5520
Db	5461	AATGATGCTACAGCTGTGTGTGCTTCTGTGTGTAAGGAGAGCTTTCATCATTCACCTCTTG	5520
QY	5521	GCACAGAGTGCACCAATGTTGGTGTGTGAGCCAGATGCTCTGAGACAGAGGACAAATGGCT	5580
Db	5521	GCACAGAGTGCACCAATGTTGGTGTGTGAGCCAGATGCTCTGAGACAGAGGACAAATGGCT	5580
QY	5581	TCCATGCAATTTGGGACAGATGTGTGAGGACACTGTGTGACCCGAGAGTGGGTGTGACA	5640
Db	5581	TCCATGCAATTTGGGACAGATGTGTGAGGACACTGTGTGACCCGAGAGTGGGTGTGACA	5640
QY	5641	GTTAGAGACTCTACCAAGTGCAGAGAGTGGACACCTACTGTATACCCAGATCCCCACA	5700
Db	5641	GTTAGAGACTCTACCAAGTGCAGAGAGTGGACACCTACTGTATACCCAGATCCCCACA	5700

Query Match	Best Local Similarity	Score	DB 1	Length	5711
Matches	5710	Conservative	1	Mismatches	0
				Indels	Gaps
QY 1	AGCTGCGTGAACACTTCTCGAGACCCCGACACAGGCGTGTGGGTTTTCGATTAACGTGGCC	60			
DB 1	AGCTGCGTGAACACTTCTCGAGACCCCGACACAGGCGTGTGGGTTTTCGATTAACGTGGCC	60			
QY 61	CTGTGGCGTCAAGAGAGCCCTTCAACCCCTGCTCGGTGAAGTTCATTGGAAACGAAGAATA	120			
DB 61	CTGTGGCGTCAAGAGAGCCCTTCAACCCCTGCTCGGTGAAGTTCATTGGAAACGAAGAATA	120			
QY 121	TGATTTATCTGCTCTTTCGCGCTTGAAGAAGTACAAATGTCAATTAATCTATGACGAATA	180			
DB 121	TGATTTATCTGCTCTTTCGCGCTTGAAGAAGTACAAATGTCAATTAATCTATGACGAATA	180			
QY 181	TCTTAGAGTGTCCCATCTGTCTGAGAGTTCAGACAGGACCTGTCTCCACCAAAAGTGTGACC	240			
DB 181	TCTTAGAGTGTCCCATCTGTCTGAGAGTTCAGACAGGACCTGTCTCCACCAAAAGTGTGACC	240			



Db 2401 AAGATCTGTAGAGAGTAGACGATTTTCATTGGTACCTGGTACTGATTATGCGACTAGG 2460  
QY 2461 AAGATCTGTAGAGAGTAGACGATTTTCATTGGTACCTGGTACTGATTATGCGACTAGG 2520  
Db 2461 AAGATCTGTAGAGAGTAGACGATTTTCATTGGTACCTGGTACTGATTATGCGACTAGG 2520  
QY 2521 GTGTGATCTGATGTGCGACGATTTTAAACCCTGAAGGAGCTTAATCATGTTGTTCCAAAG 2580  
Db 2521 GTGTGATCTGATGTGCGACGATTTTAAACCCTGAAGGAGCTTAATCATGTTGTTCCAAAG 2580  
QY 2581 ATATATGAATATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCACAGTC 2640  
Db 2581 ATATATGAATATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCACAGTC 2640  
QY 2641 GGGAAACAGCATGAGAAATGGAAGAAAGTGAATGCTGCTAGTATTGTCAGATACAT 2700  
Db 2641 GGGAAACAGCATGAGAAATGGAAGAAAGTGAATGCTGCTAGTATTGTCAGATACAT 2700  
QY 2701 TCAAGGTTTCAAGCGCGCAGTATTGCTGCTGTTTCAATCCAGAAATGCGAGAGAGG 2760  
Db 2701 TCAAGGTTTCAAGCGCGCAGTATTGCTGCTGTTTCAATCCAGAAATGCGAGAGAGG 2760  
QY 2761 AATGTGCAACATTTCTGCGCCACTCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCGCCACTCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAGAGAGAAATCAAGAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAGAGAGAAATCAAGAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
QY 2881 AGACAGTATATATCAGTCGACGCTTCTCTGTTGTTGTCAGAAAGATTAAGCCAGTTATA 2940  
Db 2881 AGACAGTATATATCAGTCGACGCTTCTCTGTTGTTGTCAGAAAGATTAAGCCAGTTATA 2940  
QY 2941 ATGCGCAATGTAGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Db 2941 ATGCGCAATGTAGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
QY 3001 ACGAACTGAGACTTACTCTCAAAATTAACATGAGACTTTTACAAACCCATATGCTATAC 3060  
Db 3001 ACGAACTGAGACTTACTCTCAAAATTAACATGAGACTTTTACAAACCCATATGCTATAC 3060  
QY 3061 CACACACTTTTCCCATCAAGCATTTGTTAAACATTAATGTAAGAAAAATCTGCTAAGG 3120  
Db 3061 CACACACTTTTCCCATCAAGCATTTGTTAAACATTAATGTAAGAAAAATCTGCTAAGG 3120  
QY 3121 AAAACTTTGAGGAACATTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACCTGCA 3180  
Db 3121 AAAACTTTGAGGAACATTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACCTGCA 3180  
QY 3181 GTACAGTGAACACATTTAGCCGTAATTAACATTTAGAGAAAAATGTTTTAAAGAACCCAGCT 3240  
Db 3181 GTACAGTGAACACATTTAGCCGTAATTAACATTTAGAGAAAAATGTTTTAAAGAACCCAGCT 3240  
QY 3241 CAAGCATATTAATGAAGTAGTTCGAGTCAATGAAGTGGGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCATATTAATGAAGTAGTTCGAGTCAATGAAGTGGGCTCCAGTATTAATGA 3300  
QY 3301 TAGGTTCCAGTATGAAGAAATTCAGACAGAACTAGGTAGAGAAACAGAGGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAATTCAGACAGAACTAGGTAGAGAAACAGAGGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGTCTATTAACAAAGTCTTCTGGA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGTCTATTAACAAAGTCTTCTGGA 3420  
QY 3421 GTATTTTGAAGCATCTGGAATTAAGAAAGCAAGAAATGAAGAGTGTTCAGACTTTA 3480  
Db 3421 GTATTTTGAAGCATCTGGAATTAAGAAAGCAAGAAATGAAGAGTGTTCAGACTTTA 3480  
QY 3481 ATACAGATTTCTCTCATCTGATCTGATTTCAAGTAATTAAGAACAGCTATGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCATCTGATTTCAAGTAATTAAGAACAGCTATGGAAGTAGTC 3540

QY 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATAAAG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATAAAG 3600  
QY 3601 AAGATCTAGTTTGTGGAATAATGACATTAAGAAAGTCTGCTTTTACGAAAAAGC 3660  
Db 3601 AAGATCTAGTTTGTGGAATAATGACATTAAGAAAGTCTGCTTTTACGAAAAAGC 3660  
QY 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTAGCCCTTACCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTAGCCCTTACCCATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGATAGACACGCTGCTACGAGTGTCTGCTAAGAACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGGATAGACACGCTGCTACGAGTGTCTGCTAAGAACACAGAGAGATTTAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAATGACTGACGTAACCAAGTAATTTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAATGACTGACGTAACCAAGTAATTTGGCAAGGCATCTC 3960  
QY 3961 AGGAACATCACCTTATGAGAGAAACAAATGTTCTGTAAGTGTGTTTCTTCACAGTGA 4020  
Db 3961 AGGAACATCACCTTATGAGAGAAACAAATGTTCTGTAAGTGTGTTTCTTCACAGTGA 4020  
QY 4021 GTGAATTTGGAAGACTGACGCAAAATACAAACCCAGAGATCTTCTTATTTGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTGACGCAAAATACAAACCCAGAGATCTTCTTATTTGTTCTT 4080  
QY 4081 CCAACCAATGAGGACATCAGTCTGAAGCCAGAGAGTGTGCTGAGTACAGAGAAATGG 4140  
Db 4081 CCAACCAATGAGGACATCAGTCTGAAGCCAGAGAGTGTGCTGAGTACAGAGAAATGG 4140  
QY 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGACAAAGCA 4200  
Db 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGACAAAGCA 4200  
QY 4201 TGGATTTCAAATAGGTAAGAGCAGCATCTGGGTGAGAGTGAACAAGGCTCTCTGAAG 4260  
Db 4201 TGGATTTCAAATAGGTAAGAGCAGCATCTGGGTGAGAGTGAACAAGGCTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGAATTTTAAACCACTCAGAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGAATTTTAAACCACTCAGAGAGGATACCATGC 4320  
QY 4321 AACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGCTGAACATGAAGCTGTGTAAGACGC 4380  
Db 4321 AACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGCTGAACATGAAGCTGTGTAAGACGC 4380  
QY 4381 ATGGAGACCGACCTCTTCAACAGTACCCCTTCATCAATTAAGTACTCTTGGCCCTTGAGG 4440  
Db 4381 ATGGAGACCGACCTCTTCAACAGTACCCCTTCATCAATTAAGTACTCTTGGCCCTTGAGG 4440  
QY 4441 ACCTGGGAAATTCAGAAACAAAGCAGATCAGAAAAAGCAGATTAATTAAGTCAAGAAAAAGTA 4500  
Db 4441 ACCTGGGAAATTCAGAAACAAAGCAGATCAGAAAAAGCAGATTAATTAAGTCAAGAAAAAGTA 4500  
QY 4501 GTGAATTAACCTTAATTAAGCCAGAAATTCAGAGAGGCTTCTGCTGAAGTTGAGAGTCTG 4560  
Db 4501 GTGAATTAACCTTAATTAAGCCAGAAATTCAGAGAGGCTTCTGCTGAAGTTGAGAGTCTG 4560  
QY 4561 CAGATAGTTCTTACAGTAAATAAAGAAACAGAGTGAAGAAAGTATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTTACAGTAAATAAAGAAACAGAGTGAAGAAAGTATCCCTTCTTAAT 4620

Oy	4621	GGCCATCATTAAGTATGATGGTGGACATGTGCACATGTCGCTCGTGGAGTCTTCAGATATAGA	4680
Db	4621	GGCCATCATTAAGTATGATGGTGGACATGTGCACATGTCGCTCGTGGAGTCTTCAGATATAGA	4680
Oy	4681	ACTACCATCTCAGAGAGAGCTCTTAAGGTTGTATGTGGAGAGCACAGCTGGAG	4740
Db	4681	ACTACCATCTCAGAGAGAGCTCTTAAGGTTGTATGTGGAGAGCACAGCTGGAG	4740
Oy	4681	ACTACCATCTCAGAGAGAGCTCTTAAGGTTGTATGTGGAGAGCACAGCTGGAG	4740
Db	4681	ACTACCATCTCAGAGAGAGCTCTTAAGGTTGTATGTGGAGAGCACAGCTGGAG	4740
Oy	4741	AGTCTGGGGCACAGATTTTACGGAAACATCTTACTGGCCAAAGGCAGATCTAGAGGGA	4800
Db	4741	AGTCTGGGGCACAGATTTTACGGAAACATCTTACTGGCCAAAGGCAGATCTAGAGGGA	4800
Oy	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTCTCTGTATGACCCCTGAATCTGATCCCTCTG	4860
Db	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTCTCTGTATGACCCCTGAATCTGATCCCTCTG	4860
Oy	4861	AAGACAGACCCCCAGAGTACGCTCTGTGTGGCAATACCATCTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGACCCCCAGAGTACGCTCTGTGTGGCAATACCATCTTCAACCTCTGATTTGA	4920
Oy	4921	AAGTCCCAATTTGAAGTTGACGAATCTCCAGATCTCCAGTCCAGCTGCTCATACTG	4980
Db	4921	AAGTCCCAATTTGAAGTTGACGAATCTCCAGATCTCCAGATCTCCAGTCTGCTCATACTG	4980
Oy	4981	ATACCTCTGGGTATTAATGCATGGAAGAAAGTGTGACAGAGGAGAACCCAAATTTGACG	5040
Db	4981	ATACCTCTGGGTATTAATGCATGGAAGAAAGTGTGACAGAGGAGAACCCAAATTTGACG	5040
Oy	5041	CTTCAACAGAAAGGTCACAAAAGAAATGTCATGATGGTGTGGGCTGAGCCCCAGAG	5100
Db	5041	CTTCAACAGAAAGGTCACAAAAGAAATGTCATGATGGTGTGGGCTGAGCCCCAGAG	5100
Oy	5101	AATTTATGCTGTGTACAGATTTGCCGAAAACACACATCATTTAATTAATTA	5160
Db	5101	AATTTATGCTGTGTGTACAGATTTGCCGAAAACACACATCATTTAATTAATTA	5160
Oy	5161	CTGAAGAGACTACTCATGTGTATGAAAACAGATGCTGAGTTGTGTGTGAAGGACAC	5220
Db	5161	CTGAAGAGACTACTCATGTGTGTATGAAAACAGATGCTGAGTTGTGTGTGAAGGACAC	5220
Oy	5221	TGAAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTAGCTATTTTGGGCTGACCC	5280
Db	5221	TGAAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTAGCTATTTTGGGCTGACCC	5280
Oy	5281	AGCTTATTTAAAGAAAATAATGCTGAATAGCATATTTTGAAGTACAGAGAGATGTGG	5340
Db	5281	AGCTTATTTAAAGAAAATAATGCTGAATAGCATATTTTGAAGTACAGAGAGATGTGG	5340
Oy	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGGAGACAAAGAAATGCCAGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGGAGACAAAGAAATGCCAGACAGAAAGATCT	5400
Oy	5401	TCAGGGGGCTAGAAATCTGTGCTATGAGGCCCTTACCAACATGCCCCAGATCAATGCG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTGCTATGAGGCCCTTACCAACATGCCCCAGATCAATGCG	5460
Oy	5461	AATGATGTGTACAGCTGTGGGTGCTCTGTGGGAAGAGCTTATCAATTCACCCCTTG	5520
Db	5461	AATGATGTGTACAGCTGTGGGTGCTCTGTGGGAAGAGCTTATCAATTCACCCCTTG	5520
Oy	5521	GCACAGGTGTCCACCAATTTGTGTGTGTGACGACAGATGCTGTGACAGAGACAATGGCT	5580
Db	5521	GCACAGGTGTCCACCAATTTGTGTGTGTGACGACAGATGCTGTGACAGAGACAATGGCT	5580
Oy	5581	TCACATGCAATTTGGGCGAGTGTGTGAGGACACTGTGTGGTGTGGTGTGGTGTGGACA	5640
Db	5581	TCACATGCAATTTGGGCGAGTGTGTGAGGACACTGTGTGGTGTGGTGTGGTGTGGACA	5640
Oy	5641	GTTGTAGCACTTACACAGTCCAGAGACTGTGACACTGATACCCAGATCCCCCACA	5700
Db	5641	GTTGTAGCACTTACACAGTCCAGAGACTGTGACACTGATACCCAGATCCCCCACA	5700
Oy	5701	GGCACTACTGCA 5711	5760

Db	5701 GCCACTACTGCA 5711	
RESULT	8	
ID	V46461 standard; cDNA: 5711 BP.	V46461
AC	V46461;	
DT	18-NOV-1998 (first entry)	
DE	Human BRCA1 om12 polymorphism #4 cDNA.	
RM	BRCA1; om12; human; breast and ovarian cancer predisposing gene;	
KW	polymorphism; susceptibility; anti-oncogene; tumour suppressor;	
OS	chromosome 17q; ss.	
RS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	120..5711
FT		/*tag- a
FT	variation	/product= "BRCA1 om12 protein"
FT		3232
FT		/*tag- b
FT		/note= "this polymorphic variation can be an A or G nucleotide"
PN	US5750400-A.	
PD	12-MAY-1998.	
PR	12-FEB-1997; 798691.	
PR	12-FEB-1996; US-598591.	
PR	12-FEB-1997; US-798691.	
PA	(OMCO-) ONCORMED INC.	
PI	Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,	
PI	Schelter DB, Zeng B;	
PI	WPI; 98-296774/26.	
PT	BRCA1 om1 gene coding sequences - useful for distinguishing between	
PT	polymorphisms and mutation(s) in the screening for disposition to	
PT	breast or ovarian cancer	
PS	Claim 2e; Page -; 54pp; English.	
CC	This sequence encodes a human BRCA1 (breast and ovarian cancer	
CC	predisposing gene) om12 gene in which a polymorphic variation occurs at	
CC	nucleotide 3235. This sequence and other polymorphic variations of this	
CC	sequence are useful for the identification of an individual who may or	
CC	may not have an increased susceptibility to breast or ovarian cancer.	
CC	The sequences used identify gene changes which are due to polymorphisms,	
CC	rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour	
CC	suppressor) which is involved in genetic inheritance of cancers,	
CC	especially breast and ovarian cancer. It is found at human chromosome 17q	
CC	which is known to be linked to cancer susceptibility, especially breast	
CC	cancer. Cells containing a mutation in this gene lose the wild-type	
CC	function of BRCA1 and are more susceptible to cancers.	
CC	NOTE: This sequence does not appear in the specification but has been	
CC	created from the wild type BRCA1 om12 gene represented in V46449.	
SO	Sequence 5711 BP; 1955 A; 1098 C; 1274 G; 1383 T;	
Query Match	100.0%; Score 5710.6; DB 1; Length 5711;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 5710; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AGCTCGCTGAGAACTTCTCTGGACCCCGGACACAGCGTGTGGGGTTCTTCAATTAATGGGCC	60
DB	1 AGCTCGCTGAGAACTTCTCTGGACCCCGGACACAGCGTGTGGGGTTCTTCAATTAATGGGCC	60
QY	61 CCTGCGCTCAGAGGCGCTTACACCTCTGCTGCGGTGAAGTTCATTTGGAGACAGAAAGAA	120
DB	61 CCTGCGCTCAGAGGCGCTTACACCTCTGCTGCGGTGAAGTTCATTTGGAGACAGAAAGAA	120
QY	121 TGGATTATCTGCTCTTTCGCGTTGAAGAAATGATTCATTAAATGCTATGACAGAAA	180
DB	121 TGGATTATCTGCTCTTTCGCGTTGAAGAAATGATTCATTAAATGCTATGACAGAAA	180
QY	181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAGAAAGCAGTCTCCACAAAGGTGAC	240
DB	181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAGAAAGCAGTCTCCACAAAGGTGAC	240
QY	241 ACAATATTTCGAATTTTGCATGCTGAAGACTTCTCAACGACAGAAAGGCGCTTACAGT	300

```
|||||
Db 241 ACATATTTTGCAAATTTTGCAATGCTGAAACCTTTCACACCAACAAAGAGGGCTTCACAGT 300
QY 301 GTCCCTTATGTAAGATGATATTAACCAAAAGAGCCTTACAAAGAAAGTACGAGATTTAGTC 360
Db 301 GTCCCTTATGTAAGATGATATTAACCAAAAGAGCCTTACAAAGAAAGTACGAGATTTAGTC 360
QY 361 AACTTGTGAAGAGCTATTTGAAATTCATTTTGTCTTTACAGTTGACAGAGTTTGGAGT 420
Db 361 AACTTGTGAAGAGCTATTTGAAATTCATTTTGTCTTTACAGTTGACAGAGTTTGGAGT 420
QY 421 ATGCAACAGCTATTAATTTTGCAAAAAGAAAAATTAACCTCCCTGAACATCTAAAGATG 480
Db 421 ATGCAACAGCTATTAATTTTGCAAAAAGAAAAATTAACCTCCCTGAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTTACAGAAACCGTGCCAAAAAGACTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTTACAGAAACCGTGCCAAAAAGACTTCTACAGAGTG 540
QY 541 AACCAGAAATCCTTCTCTGCGAGAAACCACTCTCACTCTCAACTCTCTTAACCTTGGAA 600
Db 541 AACCAGAAATCCTTCTCTGCGAGAAACCACTCTCACTCTCAACTCTCTTAACCTTGGAA 600
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACCTCAAAAGACGTCTGTACATG 660
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACCTCAAAAGACGTCTGTACATG 660
QY 661 AATTGGATCTGATCTCTCTGAGATACCGTTAATAAAGCAACTTATTTGCACTGTGGAG 720
Db 661 AATTGGATCTGATCTCTCTGAGATACCGTTAATAAAGCAACTTATTTGCACTGTGGAG 720
QY 721 ATCAAGATTTGTACAATCAACCCCTCAAGSACCAAGGAGTGAATCACTTTGATTTCTG 780
Db 721 ATCAAGATTTGTACAATCAACCCCTCAAGSACCAAGGAGTGAATCACTTTGATTTCTG 780
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATTAACAATACGAAATCATATCAAC 840
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATTAACAATACGAAATCATATCAAC 840
QY 841 CCAGTAAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAAAGT 900
Db 841 CCAGTAAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAAAGT 900
QY 901 ATCAAGGATGCTTCTGTTCAAACTTGCATGTGAGCCATGTGGCACAAAATCTCATGCCA 960
Db 901 ATCAAGGATGCTTCTGTTCAAACTTGCATGTGAGCCATGTGGCACAAAATCTCATGCCA 960
QY 961 GCTCATTAACAGATGAGAGACAGAGTTTATTAACACATAAGAGAGATGAATGTAGAAA 1020
Db 961 GCTCATTAACAGATGAGAGACAGAGTTTATTAACACATAAGAGAGATGAATGTAGAAA 1020
QY 1021 AAGCTGAATTTCTGTAATAAAGCAAAACAGCTGGCTTACAGAGAGCCACATTAACAGAT 1080
Db 1021 AAGCTGAATTTCTGTAATAAAGCAAAACAGCTGGCTTACAGAGAGCCACATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCCAAGACAGAAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCCAAGACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAAAGATGGAATTAAGAGAAATGCGATGCT 1200
Db 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAAAGATGGAATTAAGAGAAATGCGATGCT 1200
QY 1201 CAGAGAAATCTAGAGATACTGAAGATGTTCTTGATTAACATAATTAAGCAGCATTCGA 1260
Db 1201 CAGAGAAATCTAGAGATACTGAAGATGTTCTTGATTAACATAATTAAGCAGCATTCGA 1260
QY 1261 AAGTTAATGATGTTTCCAGAAAGTATGAACGTTAAGGTTTCAATGATCAATGATG 1320
Db 1261 AAGTTAATGATGTTTCCAGAAAGTATGAACGTTAAGGTTTCAATGATCAATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTGAATGATGGAGCTTAAATGAGGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTGAATGATGGAGCTTAAATGAGGTAGATG 1380
|||||

Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGATGGAGCTTAAATGAGGTAGATG 1380
QY 1381 AATATTTGCTTCTCAGAGAAAAATAGACTTACTGGCCAGTGAATCTCATGAGGCTTTAA 1440
Db 1381 AATATTTGCTTCTCAGAGAAAAATAGACTTACTGGCCAGTGAATCTCATGAGGCTTTAA 1440
QY 1441 TATGTAAGGAAAGAGTTTCACTCCCAATCAGTAGAGAGTAATTAATGAAGACAAAATAT 1500
Db 1441 TATGTAAGGAAAGAGTTTCACTCCCAATCAGTAGAGAGTAATTAATGAAGACAAAATAT 1500
QY 1501 TTGGGAAACCTATCGAGAGAAAGGCAAGCCCTCCCACTTAAGCCATGTAACCTGAAATC 1560
Db 1501 TTGGGAAACCTATCGAGAGAAAGGCAAGCCCTCCCACTTAAGCCATGTAACCTGAAATC 1560
QY 1561 TAAATTAAGAGCATTTTGTACTGAGCCACAGATTAATACAAGAGCGTCCCTCAAAATA 1620
Db 1561 TAAATTAAGAGCATTTTGTACTGAGCCACAGATTAATACAAGAGCGTCCCTCAAAATA 1620
QY 1621 AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTCAATCCCTGAGAGATTTATCAAGAAAG 1680
Db 1621 AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTCAATCCCTGAGAGATTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAAAATGATTAATCAAGGAACTAACCAACGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAAAATGATTAATCAAGGAACTAACCAACGAGC 1740
QY 1741 AGAATGGTCAAGTATGATTAATTAATAGTGTGATGAGATTAACAAAGAGTGATT 1800
Db 1741 AGAATGGTCAAGTATGATTAATTAATAGTGTGATGAGATTAACAAAGAGTGATT 1800
QY 1801 CTATTCGAATGAGAAAAATTCCTAACCCATAGAAATCACTCGAAAAAGAAATCTGTTCA 1860
Db 1801 CTATTCGAATGAGAAAAATTCCTAACCCATAGAAATCACTCGAAAAAGAAATCTGTTCA 1860
QY 1861 AAAGGAAAGCTGAACCTATTAAGCAGAGTAAATCAATATGAACTGAATTAATATTC 1920
Db 1861 AAAGGAAAGCTGAACCTATTAAGCAGAGTAAATCAATATGAACTGAATTAATATTC 1920
QY 1921 ACAATTCAAAAAGCACCTAAAAAGATAGGCTGAGAGGAAAGTCTTCAACGAGCATATTC 1980
Db 1921 ACAATTCAAAAAGCACCTAAAAAGATAGGCTGAGAGGAAAGTCTTCAACGAGCATATTC 1980
QY 1981 ATGCGCTTGAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Db 1981 ATGCGCTTGAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
QY 2041 TTGATAGTTGTTCTAGAGAGTAAGAGATTAAGAAAAAAGTAAACCAATGACAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGAGAGTAAGAGATTAAGAAAAAAGTAAACCAATGACAGTCA 2100
QY 2101 GGCACAGCAGAAACCTCAACTCATGAGAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
Db 2101 GGCACAGCAGAAACCTCAACTCATGAGAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
QY 2161 GTAAACAAGCCAAATGAACAGACAGTAAGAAAGACATGACAGGATCTTCCAGAGCTGA 2220
Db 2161 GTAAACAAGCCAAATGAACAGACAGTAAGAAAGACATGACAGGATCTTCCAGAGCTGA 2220
QY 2221 AGTTAAACAAATGACACCTGGTCTTCTTACTAAGTGTCAAAATACCAAGTAAAGAT 2280
Db 2221 AGTTAAACAAATGACACCTGGTCTTCTTACTAAGTGTCAAAATACCAAGTAAAGAT 2280
QY 2281 TTGTCAATCTAGCCTTCAAGAGAGAAAAAGAGAAAACTAGAAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTAGCCTTCAAGAGAGAAAAAGAGAAAACTAGAAAACAGTTAAAGTGT 2340
QY 2341 CTATTAATGCTGAAGAGACCCCAAGATCTCATGTTAATGAGAAAGGTTTGGAAACTG 2400
Db 2341 CTATTAATGCTGAAGAGACCCCAAGATCTCATGTTAATGAGAAAGGTTTGGAAACTG 2400
QY 2401 AAAGATCTGTAGAGAGTAGAGATTTTCAATGAGTGTGAGTACTGATTAATGAGCCTAGG 2460
Db 2401 AAAGATCTGTAGAGAGTAGAGATTTTCAATGAGTGTGAGTACTGATTAATGAGCCTAGG 2460
|||||
```



OY 2461 AAGATCTCGTACTGGAAGTTAGCACTTAGGGAAGCCAAAAACAGAACCAATAAT 2520  
|||||  
DB 2461 AAGATCTCGTACTGGAAGTTAGCACTTAGGGAAGCCAAAAACAGAACCAATAAT 2520  
OY 2521 GGTGAGTCAGTGTGGCAGCAATTTGAAAAACCCAGAGCACTAATTCATGTTGTTCCAAAG 2580  
|||||  
DB 2521 GGTGAGTCAGTGTGGCAGCAATTTGAAAAACCCAGAGCACTAATTCATGTTGTTCCAAAG 2580  
OY 2581 ATAAATGAATGACACAGAAAGGCTTAAAGTATCCATTGGGACATGAATTAACACAGTC 2640  
|||||  
DB 2581 ATAAATGAATGACACAGAAAGGCTTAAAGTATCCATTGGGACATGAATTAACACAGTC 2640  
OY 2641 GGGAAACACAGATGAAGATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCGAATACAT 2700  
|||||  
DB 2641 GGGAAACACAGATGAAGATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCGAATACAT 2700  
OY 2701 TCAGGTTTTCAAGCGCCAGTCATTTGCTGTTCATAATCCAGAAATGCGAAGAG 2760  
|||||  
DB 2701 TCAGGTTTTCAAGCGCCAGTCATTTGCTGTTCATAATCCAGAAATGCGAAGAG 2760  
OY 2761 AATGTCCAAACATTTCTGTGCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
|||||  
DB 2761 AATGTCCAAACATTTCTGTGCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
OY 2821 TTGAATGTGAACAAAGGAAGAAATATCAGGAAGAAATGAGTCTAATATCAAGCCTGTAC 2880  
|||||  
DB 2821 TTGAATGTGAACAAAGGAAGAAATATCAGGAAGAAATGAGTCTAATATCAAGCCTGTAC 2880  
OY 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTGGTGGTCAAGAAATGAGCAATGATA 2940  
|||||  
DB 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTGGTGGTCAAGAAATGAGCAATGATA 2940  
OY 2941 ATGCCAAATGTACTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA 3000  
|||||  
DB 2941 ATGCCAAATGTACTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA 3000  
OY 3001 AGGAACCTGACATCTACTACCAATTAACATGAGACTTTTACAAACCCATATGCTATAC 3060  
|||||  
DB 3001 AGGAACCTGACATCTACTACCAATTAACATGAGACTTTTACAAACCCATATGCTATAC 3060  
OY 3061 CACCACTTTTCCCATCAAGTCAATTTGTAAACTAATGTAAAGAAATCTGCTAGAG 3120  
|||||  
DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTAAACTAATGTAAAGAAATCTGCTAGAG 3120  
OY 3121 AAAACTTTAGGAACATTCATGTCACTGAAAGAGAAATGGGAATGAGAACATTTCCAA 3180  
|||||  
DB 3121 AAAACTTTAGGAACATTCATGTCACTGAAAGAGAAATGGGAATGAGAACATTTCCAA 3180  
OY 3181 GTACAGTGAAGCAATTTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
|||||  
DB 3181 GTACAGTGAAGCAATTTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
OY 3241 CAAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300  
|||||  
DB 3241 CAAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300  
OY 3301 TAGGTTCCAGTGTAAACATTCAGAGCAAGTCTAGTAGAAACAGAGGCCCAAAATGTA 3360  
|||||  
DB 3301 TAGGTTCCAGTGTAAACATTCAGAGCAAGTCTAGTAGAAACAGAGGCCCAAAATGTA 3360  
OY 3361 ATGCTATGCTTAGATTAGAGGTTTTGCAACCTTAGAGTCTAATAACAAAGTCTTCTGGA 3420  
|||||  
DB 3361 ATGCTATGCTTAGATTAGAGGTTTTGCAACCTTAGAGTCTAATAACAAAGTCTTCTGGA 3420  
OY 3421 GTAATTTAGCATCCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGAGCTTA 3480  
|||||  
DB 3421 GTAATTTAGCATCCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGAGCTTA 3480  
OY 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTAAAGTCAAGCCTATGGAAGTAGTCT 3540  
|||||  
DB 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTAAAGTCAAGCCTATGGAAGTAGTCT 3540

OY 3541 ATGCATCTCAGGTTTTGTTGAGACACCTGATGACCTGTTAGATGATGTAATTAAG 3600  
|||||  
DB 3541 ATGCATCTCAGGTTTTGTTGAGACACCTGATGACCTGTTAGATGATGTAATTAAG 3600  
OY 3601 AAGTACTAGTTTTGCGAATAATGACATTAAGGAAGTCTGCTGTTTTTACGAAGAGC 3660  
|||||  
DB 3601 AAGTACTAGTTTTGCGAATAATGACATTAAGGAAGTCTGCTGTTTTTACGAAGAGC 3660  
OY 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTTAGCCCTTTCACCCATACACTTTGGCTCAG 3720  
|||||  
DB 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTTAGCCCTTTCACCCATACACTTTGGCTCAG 3720  
OY 3721 GTTACCAAGAGGGGCCAAGAAATTAGAGTCTCAAGAGAACTTATAGTAGAGATG 3780  
|||||  
DB 3721 GTTACCAAGAGGGGCCAAGAAATTAGAGTCTCAAGAGAACTTATAGTAGAGATG 3780  
OY 3781 AAGAGCTTCCCTGCTTCAACACCTGTTATTTGTTAAAGTAAACATTAATACCTTCAGT 3840  
|||||  
DB 3781 AAGAGCTTCCCTGCTTCAACACCTGTTATTTGTTAAAGTAAACATTAATACCTTCAGT 3840  
OY 3841 CTACTAGCATAGCACCGTTGCTACCGAGTGTCTCTAAGAACACAGAGAGAAATTAAT 3900  
|||||  
DB 3841 CTACTAGCATAGCACCGTTGCTACCGAGTGTCTCTAAGAACACAGAGAGAAATTAAT 3900  
OY 3901 TATCATTTGAAGAAATAGCTTAATGACTGCAATACCGAGTAAATTTGGCAAGGCATCTC 3960  
|||||  
DB 3901 TATCATTTGAAGAAATAGCTTAATGACTGCAATACCGAGTAAATTTGGCAAGGCATCTC 3960  
OY 3961 AGGAATCACTACCTTAGTGAAGAAACAAATGTTCTGCTAGCTTGTTCCTACAGTGA 4020  
|||||  
DB 3961 AGGAATCACTACCTTAGTGAAGAAACAAATGTTCTGCTAGCTTGTTCCTACAGTGA 4020  
OY 4021 GTGAATTTGAAGAACTTACTGCAATATCAAAACACCGAGATCTTCTGATTTGTTCTT 4080  
|||||  
DB 4021 GTGAATTTGAAGAACTTACTGCAATATCAAAACACCGAGATCTTCTGATTTGTTCTT 4080  
OY 4081 CCAAAACAAATGAGGCATCACTGTAAGAGCCAGGAGTTGTTGAGTGAACAGAAATGG 4140  
|||||  
DB 4081 CCAAAACAAATGAGGCATCACTGTAAGAGCCAGGAGTTGTTGAGTGAACAGAAATGG 4140  
OY 4141 TTTGAGTGAATGAAGAAAGAGAAAGGCTTGAAGAAATTAATCAAGAAAGCAACGA 4200  
|||||  
DB 4141 TTTGAGTGAATGAAGAAAGAGAAAGGCTTGAAGAAATTAATCAAGAAAGCAACGA 4200  
OY 4201 TGGATTTCAAACCTTAGTGAAGCAGATCTGGGTGTGAGAGTGAACAAAGCCTCTGAAG 4260  
|||||  
DB 4201 TGGATTTCAAACCTTAGTGAAGCAGATCTGGGTGTGAGAGTGAACAAAGCCTCTGAAG 4260  
OY 4261 ACTGCTCAGGGGCTATCTCTCAGAGTGAATTTTAACCACTGAGAGAGGATACCATGC 4320  
|||||  
DB 4261 ACTGCTCAGGGGCTATCTCTCAGAGTGAATTTTAACCACTGAGAGAGGATACCATGC 4320  
OY 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGACCTGTTAGAAACAGC 4380  
|||||  
DB 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGACCTGTTAGAAACAGC 4380  
OY 4381 ATGGAGCCAGCCCTTCTAACAGCTACCTTCATCATTAAGTACTCTTGCCTTGAAG 4440  
|||||  
DB 4381 ATGGAGCCAGCCCTTCTAACAGCTACCTTCATCATTAAGTACTCTTGCCTTGAAG 4440  
OY 4441 ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTCACAGAAAAATA 4500  
|||||  
DB 4441 ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTCACAGAAAAATA 4500  
OY 4501 GTGAATACCTTTAAGCCGAATTCAGAAAGGCTTCTGCTGACAGAAAGTTAGAGTGTG 4560  
|||||  
DB 4501 GTGAATACCTTTAAGCCGAATTCAGAAAGGCTTCTGCTGACAGAAAGTTAGAGTGTG 4560  
OY 4561 CAGATAGTTCTACAGATTAATAAGAAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
|||||  
DB 4561 CAGATAGTTCTACAGATTAATAAGAAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
OY 4621 GCCCATCATTAATGATGATGAGTGTGCTACATGACAGTTGCTTGGGAGTCTTCAAGATGA 4680





```
Db 241 ACATATTTTCCAAATTTTGCATGCTGAAACTTTCACACAGAGAAAGGCCCTTACACT 300
QY 301 GTGCTTATGTAGAAATGATATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTTAGTC 360
Db 301 GTGCTTATGTAGAAATGATATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTTAGTC 360
QY 361 AACTTGTGAAGAGCTATTGAAAATCATTTTGTCTTTTACGCTTGACAGAGTTTGAGAT 420
Db 361 AACTTGTGAAGAGCTATTGAAAATCATTTTGTCTTTTACGCTTGACAGAGTTTGAGAT 420
QY 421 ATGCAAAACAGCTATTAATTTGCAAAAAGAAAATACTCTCTGAACATCTAAAGATG 480
Db 421 ATGCAAAACAGCTATTAATTTGCAAAAAGAAAATACTCTCTGAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGATTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGATTCTACAGAGTG 540
QY 541 AACCCGAAAATCCTCTCTGACAGAAACAGCTCTCACTGCTCAACTCTTAACCTTGGAA 600
Db 541 AACCCGAAAATCCTCTCTGACAGAAACAGCTCTCACTGCTCAACTCTTAACCTTGGAA 600
QY 601 CTGTGAGAACTGTAGAGACAAAGCAGGAGATACAACTCAAAAGAGCTGTCTACATTTG 660
Db 601 CTGTGAGAACTGTAGAGACAAAGCAGGAGATACAACTCAAAAGAGCTGTCTACATTTG 660
QY 661 AATTGGAGATCTGATTTCTTCTGAAAGATACCGTTAATAAAGCACTTATTGCAGTGGAG 720
Db 661 AATTGGAGATCTGATTTCTTCTGAAAGATACCGTTAATAAAGCACTTATTGCAGTGGAG 720
QY 721 ATCAAGAAATGTTACAAATACCCCTCAAGGAACAGGAGTGAATGATTTGATTTCTG 780
Db 721 ATCAAGAAATGTTACAAATACCCCTCAAGGAACAGGAGTGAATGATTTGATTTCTG 780
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGCGATGTACAAATACTGAAATCATGATCAAC 840
Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGCGATGTACAAATACTGAAATCATGATCAAC 840
QY 841 CCAATTAATTAATGATTTTGAACACCACTGAGAAAGCTGCAGCTGAGAGGCTACAGAAAAAT 900
Db 841 CCAATTAATTAATGATTTTGAACACCACTGAGAAAGCTGCAGCTGAGAGGCTACAGAAAAAT 900
QY 901 ATCAGGAGTGTCTGTTTCAAACTGATGAGAGCCATGGGACCAAAATCTCATGCCA 960
Db 901 ATCAGGAGTGTCTGTTTCAAACTGATGAGAGCCATGGGACCAAAATCTCATGCCA 960
QY 961 GCTCATTAAGCATGAGAACAGCAGTTATTACTCACTAAAGACAGATGATAGAAA 1020
Db 961 GCTCATTAAGCATGAGAACAGCAGTTATTACTCACTAAAGACAGATGATAGAAA 1020
QY 1021 AAGGCTAATTTCTGTAATTAAGCAAGCCTGGCTTTAGCAAGAGGCCAATCAACAGAT 1080
Db 1021 AAGGCTAATTTCTGTAATTAAGCAAGCCTGGCTTTAGCAAGAGGCCAATCAACAGAT 1080
QY 1081 GGGGCTGAAGTAAAGAAACATGTAATGATAGGGGACTCCAGACAGAAAAAAGGTAG 1140
Db 1081 GGGGCTGAAGTAAAGAAACATGTAATGATAGGGGACTCCAGACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAGATGAAATAGCAGAAATGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAGATGAAATAGCAGAAATGCCATGCT 1200
QY 1201 CAGAGAAATCTAGAGATCTGAAAGATGTTCTTGGATTAACATTAATAGCAGATTGAGA 1260
Db 1201 CAGAGAAATCTAGAGATCTGAAAGATGTTCTTGGATTAACATTAATAGCAGATTGAGA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAACGTGATGAGTGTGAGATCTCAATGATG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAACGTGATGAGTGTGAGATCTCAATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTGATTAATGAGAGTCTTAAATGAGGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTGATTAATGAGAGTCTTAAATGAGGTAGATG 1380

QY 1381 AATATCTGTTCTTGAGAGAAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA 1440
Db 1381 AATATCTGTTCTTGAGAGAAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCACTAAGAGTAAATATTGAAGCAAAATAT 1500
Db 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCACTAAGAGTAAATATTGAAGCAAAATAT 1500
QY 1501 TTGGGAAAACCTATCGGAGAAAGGCAAGCCCTCCCACTTAAGCCATGATAGTAAATC 1560
Db 1501 TTGGGAAAACCTATCGGAGAAAGGCAAGCCCTCCCACTTAAGCCATGATAGTAAATC 1560
QY 1561 TAAATTAAGAGCATTTGTTACTGAGCCACAGATTAATACAGAGGCTCCCTCACAAATA 1620
Db 1561 TAAATTAAGAGCATTTGTTACTGAGCCACAGATTAATACAGAGGCTCCCTCACAAATA 1620
QY 1621 AATTAAAGCCTAAAGAGAGCCCTACAGAGCCCTGATCATCTGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAAGCCTAAAGAGAGCCCTACAGAGCCCTGATCATCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAAGAGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAAGAGAGC 1740
QY 1741 AGAATGGTCAAGTATGATTAATTTACTAATAGTGTGATGAGTAATTAACAAAGTGAT 1800
Db 1741 AGAATGGTCAAGTATGATTAATTTACTAATAGTGTGATGAGTAATTAACAAAGTGAT 1800
QY 1801 CTATTCGAATGAGAAAAATCCCTAACCCAAATGAAATCACTCCGAAAAAGATGCTTTCA 1860
Db 1801 CTATTCGAATGAGAAAAATCCCTAACCCAAATGAAATCACTCCGAAAAAGATGCTTTCA 1860
QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATCC 1920
Db 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATCC 1920
QY 1921 ACAATTTAAAAGCACTTAAGAAATAGGCTGAGAGGAAATCTTCTACAGGCAATATTC 1980
Db 1921 ACAATTTAAAAGCACTTAAGAAATAGGCTGAGAGGAAATCTTCTACAGGCAATATTC 1980
QY 1981 ATGGGCTGAAGTATGATGATGATGATTAAGCCCACTTAATGATGATGATGATGCAAA 2040
Db 1981 ATGGGCTGAAGTATGATGATGATGATTAAGCCCACTTAATGATGATGATGATGCAAA 2040
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTACCAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTACCAACCAATGCCAGTCA 2100
QY 2101 GGCACAGCAGAAAACCTACAACTCATGGAAGGTAAAGAAACCTCACTGAGGCAAGAA 2160
Db 2101 GGCACAGCAGAAAACCTACAACTCATGGAAGGTAAAGAAACCTCACTGAGGCAAGAA 2160
QY 2161 GTPAACAAAGCCAAATGAACAGACAAATGAAGAAAGATGACAGATCTTCCAGAGCTGA 2220
Db 2161 GTPAACAAAGCCAAATGAACAGACAAATGAAGAAAGATGACAGATCTTCCAGAGCTGA 2220
QY 2221 AGTTAACAAATGACACCTGCTTCTTACTAAGTGTCAATACACAGTAAATGAAGAT 2280
Db 2221 AGTTAACAAATGACACCTGCTTCTTACTAAGTGTCAATACACAGTAAATGAAGAT 2280
QY 2281 TTGTCAATCTGAGCTTCCAGAGAAAGAAAGAAAGAAAGAAATACAGAAAGTAAAGTGT 2340
Db 2281 TTGTCAATCTGAGCTTCCAGAGAAAGAAAGAAAGAAAGAAATACAGAAAGTAAAGTGT 2340
QY 2341 CTATTAATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCAGAAATG 2400
Db 2341 CTATTAATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCAGAAATG 2400
QY 2401 AAAGATCTGTAGAGATACAGATATTTCAATGATGATGATGATGATGATGATGATGATG 2460
Db 2401 AAAGATCTGTAGAGATACAGATATTTCAATGATGATGATGATGATGATGATGATGATG 2460
```

OY	2461	AAATGATCTGGTACACGAGAGTTAGACACTCTACGGAGGCAAAACAGACCAAAATTAAT	2520
Db	2461	AAAGTATCTGGTACTGGAAGTTAGACACTCTACGGAGGCAAAACAGACCAAAATTAAT	2520
OY	2521	GTTGAGTCAAGTGTGCAGCATTTTGAAAACCCCAAGGAGCATTAATTCATGGTGTGCCAAG	2580
Db	2521	GTTGAGTCAAGTGTGCAGCATTTTGAAAACCCCAAGGAGCATTAATTCATGGTGTGCCAAG	2580
OY	2581	ATATATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGACATGAAGTTAACCAAGTC	2640
Db	2581	ATATATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGACATGAAGTTAACCAAGTC	2640
OY	2641	GGGAAACACAGCATGGAATGGAGAAAAGTGAACCTTATCTCAGTATTTGGCAATTAAT	2700
Db	2641	GGGAAACACAGCATGGAATGGAGAAAAGTGAACCTTATCTCAGTATTTGGCAATTAAT	2700
OY	2701	TCAAGGTTTCAAAAGCGGCAGCTCAATTGGCTGTGTTTCAATCCAGAAAATGACAGAAAGG	2760
Db	2701	TCAAGGTTTCAAAAGCGGCAGCTCAATTGGCTGTGTTTCAATCCAGAAAATGACAGAAAGG	2760
OY	2761	AATGTGCACATTCCTCTGCCCAGCTCTGGGTCTTTAAGAAACAAAGTCCAAAAGTCATT	2820
Db	2761	AATGTGCACATTCCTCTGCCCAGCTCTGGGTCTTTAAGAAACAAAGTCCAAAAGTCATT	2820
OY	2821	TTGCAATGTGAACAAAGAGAAATCAGGAAAGATAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGCAATGTGAACAAAGAGAAATCAGGAAAGATAGTCTAATATCAAGCCTGTAC	2880
OY	2881	AGCAGATTAATATACAGCAGAGGCTTCCTGCTGCTGAGTGTGTCAGAAAGATTAAGCCAGTTGTA	2940
Db	2881	AGCAGATTAATATACAGCAGAGGCTTCCTGCTGCTGAGTGTGTCAGAAAGATTAAGCCAGTTGTA	2940
OY	2941	ATGCCAATGTAGTATCAAAAGAGAGGCTTAGTGTGTCTATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAATGTAGTATCAAAAGAGAGGCTTAGTGTGTCTATCATCTCAGTTCAGAGCA	3000
OY	3001	ACGAACTGCACTCATTTACTCTCCAAATPAACATGAGCTTTTACAAAACCCATATGCTATAC	3060
Db	3001	ACGAACTGCACTCATTTACTCTCCAAATPAACATGAGCTTTTACAAAACCCATATGCTATAC	3060
OY	3061	CACACATTTTCCCATCAATCAATCTGTTTAAACCTAAATGTAGAAAAATCTGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAATCAATCTGTTTAAACCTAAATGTAGAAAAATCTGCTAGAGG	3120
OY	3121	AAAACCTTGAGAAACATTCATCATGTCACTGTAAGAAATGGAAATGGAACATTTCCAA	3180
Db	3121	AAAACCTTGAGAAACATTCATCATGTCACTGTAAGAAATGGAAATGGAACATTTCCAA	3180
OY	3181	GTACAGTGAAGACAAATTAGCCGCTAATPAACATTAGAGAAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAAGACAAATTAGCCGCTAATPAACATTAGAGAAAATGTTTTTAAAGAGCCAGCT	3240
OY	3241	CAACCATATTAATGAAGTGAAGTGTCCAGTACTAATGAATGGGGCTCCAGTATTAATGA	3300
Db	3241	CAACCATATTAATGAAGTGAAGTGTCCAGTACTAATGAATGGGGCTCCAGTATTAATGA	3300
OY	3301	TAGTTCACAGATGAAGAAACATTCACAGAGAACTAGTGAACAACAGAGGCCCAAAATGGA	3360
Db	3301	TAGTTCACAGATGAAGAAACATTCACAGAGAACTAGTGAACAACAGAGGCCCAAAATGGA	3360
OY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCACCTGAGGCTATTAACAAAGTCTTCTGTGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCACCTGAGGCTATTAACAAAGTCTTCTGTGAA	3420
OY	3421	GTAATGTGAAGCATCCGGAATTAATAAAGCAAGAAATGAATAAGTATGTCAGACTGTTA	3480
Db	3421	GTAATGTGAAGCATCCGGAATTAATAAAGCAAGAAATGAATAAGTATGTCAGACTGTTA	3480
OY	3481	ATACAGATTTCTCTCCATATCTGATCTGATTTGAGATTAACCTATGAGGAGTATGCT	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATCTGATTTGAGATTAACCTATGAGGAGTATGCT	3540
OY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGTGATGCTGTTAAGTATGATGTGAATTAAGG	3600

D	b	3541	ATGCACTCAGGTTTGTTCTGGACACCCTGAATBACTGTTAATATATGGTGAATAAAGC	3600
O	y	3601	AAGAATTAGTTTTGCAGAAAATGACATTTAAGAAAGTTCTGCTTTTWTAGCAAACCG	3660
D	b	3601	AAGATACTAGTTTTCGCAAAATGACATTTAAGAAAGTTCTGCTTTTWTAGCAAACCG	3660
O	y	3661	TCCAGAAAGAGACCTTAGCAGAGTCTTAGCCCTTTCACCATACATTTGGCTCAGG	3720
D	b	3661	TCCAGAAAGAGAGCTTAGCAGAGAGTCTTAGCCCTTTCACCATACATTTGGCTCAGG	3720
O	y	3721	GTTACCAABAGGGGCCAANAATTAGTCTCTCAGAAGAACCTTATCTAGTAGATG	3780
D	b	3721	GTTACCCAABAGGGGCCAANAATTAGAGTCTCTCAGAAGAACCTTATCTAGTAGAGATG	3780
O	y	3781	AAGAGCTCCCTGCTTCCACAACCTGTATTTGGTAAATACATATATACCTCTCAGT	3840
D	b	3781	AAGAGCTCTCCCTGCTTCCACAACCTGTATTTGGTAAATACATATATACCTCTCAGT	3840
O	y	3841	CTACTAGGATAGACACGGTGTCTACCGAGTGTCTGTAGAACAAGAGAGAAATTTAT	3900
D	b	3841	CTACTAGGATAGACACGGTGTCTACCGAGTGTCTGTAGAACAAGAGAGAAATTTAT	3900
O	y	3901	TATCATTTGAAGAATAGCTTAAATGACTGCATPACACAGTAATATTGGCAAAGCATCTC	3960
D	b	3901	TATCATTTGAAGAATAGCTTAAATGACTGCATPACACAGTAATATTGGCAAAGCATCTC	3960
O	y	3961	AGGAACATCACCTTAGAGSAGAAACAAANTGTTGCTGCTGCTGTTTCTTCACAGTSCA	4020
D	b	3961	AGGAACATCACCTTAGAGSAGAAACAAANTGTTCTGCTGCTGTTTCTTCACAGTSCA	4020
O	y	4021	GTTGAATTTGGAAGACTTGACTGCAATATACAACACCAGGATCCTTCTTGATTGGTCTT	4080
D	b	4021	GTTGAATTTGGAAGACTTGACTGCAATATACAACACCAGGATCCTTCTTGATTGGTCTT	4080
O	y	4081	CCAAACAAATGAGGCATCACTTGAAAGCCAGGAGTTGTTGAGTGACAAAGAAATTGG	4140
D	b	4081	CCAAACAAATGAGGCATCACTTGAAAGCCAGGAGTTGTTGAGTGACAAAGAAATTGG	4140
O	y	4141	TTTAGATGATGAAAGAAAGGAAAGGGGCTTGGAAAGAAATATACAGAGCAACAAACA	4200
D	b	4141	TTTAGATGATGAAAGAAAGGAAAGGGGCTTGGAAAGAAATATATACAGAGCAACAAACA	4200
O	y	4201	TGATTTCAAACTTAGTGGAAGCAGCATCTGGGGTGAAGGTGAAGTAACAAGCGTCTTGAG	4260
D	b	4201	TGATTTCAAACTTAGTGGAAGCAGCATCTGGGGTGAAGGTGAAGTAACAAGCGTCTTGAG	4260
O	y	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGGATACCATGC	4320
D	b	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGGATACCATGC	4320
O	y	4321	AACATTAACCTGATPAAGCTCCACAGAGAAATGGCGAATACAACTGTGTAAAGAACGC	4380
D	b	4321	AACATTAACCTGATPAAGCTCCACAGAGAAATGGCGAATTAACAACTGTGTAAAGAACGC	4380
O	y	4381	ATGGAGACCAAGCTTCTTAACAGCTTCCATCATATAAGTACGCTCTGCCCCCTTGAGG	4440
D	b	4381	ATGGAGACCAAGCTTCTTAACAGCTTCCATCATATAAGTACGCTCTGCCCCCTTGAGG	4440
O	y	4441	ACCTGGCAAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGATTAATCTCACAGAAAGTA	4500
D	b	4441	ACCTGGCAAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGATTAATCTCACAGAAAGTA	4500
O	y	4501	GTTGAATACCTTATPAAGCAAGAAATCCAGAAAGGCTTCTGCTGACAAAGTTGAGGGTGTG	4560
D	b	4501	GTTGAATACCTTATPAAGCAAGAAATCCAGAAAGGCTTCTGCTGACAAAGTTGAGGGTGTG	4560
O	y	4561	CAGATAGTCTTACCAAGTAAATAAAGAACCAAGAGATGGAAGTGCATCCCCTCTTAAT	4620
D	b	4561	CAGATAGTCTTACCAAGTAAATAAAGAACCAAGAGATGGAAGTGCATCCCCTCTTAAT	4620
O	y	4621	GCCCATCATTAGATGATAGGTGTACATGCACAGTTGCTCTGGAGTCTTCAGAAATGAA	4680



Qy	241	ACATATTTTGCAAATTTTGCATGCTGAAACCTTCTCAACAGAAAGAGGCTTCCAGT	300
Db	241	ACATATTTTGGCAAAATTTTGCATGCTGAAACCTTCTCAACAGAAAGAGGCTTCCAGT	300
Qy	301	GTCCCTTATGTAGATGATTAACCAAAAGGCGCTACAGAAATAGAGATTAGTC	360
Db	301	GTCCCTTATGTAGATGATTAACCAAAAGGCGCTACAGAAATAGAGATTAGTC	360
Qy	361	AACCTTGTGAAGAGCTATGAAATCATTTGTCTTTCAGCTTGACAGATTGGAGT	420
Db	361	AACCTTGTGAAGAGCTATGAAATCATTTGTCTTTCAGCTTGACAGATTGGAGT	420
Qy	421	ATGCAAAACGCTATATTTTGCAGAAAAGAAATTAATCTCTCTGAACATTAAGATG	480
Db	421	ATGCAAAACGCTATATTTTGCAGAAAAGAAATTAATCTCTCTGAACATTAAGATG	480
Qy	481	AGTTTCTATCATCCAAATATGGGCTACAGAAACCGTGCCAAAACATCTCTCAAGTG	540
Db	481	AGTTTCTATCATCCAAATATGGGCTACAGAAACCGTGCCAAAACATCTCTCAAGTG	540
Qy	541	AACCCGAAATCCTTCTCTGCAAGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA	600
Db	541	AACCCGAAATCCTTCTCTGCAAGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA	600
Qy	601	CTGTAGAACTCTGAGGACAAAGACGGGATACACCTCAAAAAGAGCTGTCTACATTG	660
Db	601	CTGTAGAACTCTGAGGACAAAGACGGGATACACCTCAAAAAGAGCTGTCTACATTG	660
Qy	661	AATTGGATCTGATCTTCTGAAAGATACGGTTAATAAGCACTTTTTCAGAGTGGAG	720
Db	661	AATTGGATCTGATCTTCTGAAAGATACGGTTAATAAGCACTTTTTCAGAGTGGAG	720
Qy	721	ATCAAGAAATTTGTACAAATCACCCCTCAAGAAACAGGGATGAATCAGTTTGGATTCTG	780
Db	721	ATCAAGAAATTTGTACAAATCACCCCTCAAGAAACAGGGATGAATCAGTTTGGATTCTG	780
Qy	781	CAAAAAGGCTCTGTGTGAATTTTCTGAGAGCGGATTAACAAATCTGAACATCATCAAC	840
Db	781	CAAAAAGGCTCTGTGTGAATTTTCTGAGAGCGGATTAACAAATCTGAACATCATCAAC	840
Qy	841	CCAGTAATTAATGATTGTAACACACCTGAGAAACGCTGACACTGAGAGGATCCGAAAATG	900
Db	841	CCAGTAATTAATGATTGTAACACACCTGAGAAACGCTGACACTGAGAGGATCCGAAAATG	900
Qy	901	ATCAGAGTAGTCTCTTTCCTTCAAACTTGATGAGAGGCTGAGCAAAATACATGATGCA	960
Db	901	ATCAGAGTAGTCTCTTTCCTTCAAACTTGATGAGAGGCTGAGCAAAATACATGATGCA	960
Qy	961	GCTCATTCACGATGAGAAACAGCAGTTTATTACTCACTAAAGCAGAAATGAATGTGAAA	1020
Db	961	GCTCATTCACGATGAGAAACAGCAGTTTATTACTCACTAAAGCAGAAATGAATGTGAAA	1020
Qy	1021	AGGCTGAAATTCGTATATTAAGCAAAACAGCCTGCTTACCAAGAGCACAATTAACAGAT	1080
Db	1021	AGGCTGAAATTCGTATATTAAGCAAAACAGCCTGCTTACCAAGAGCACAATTAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAGAAACATGTAATGATGAGGCGACTCCACGACAGAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGAAACATGTAATGATGAGGCGACTCCACGACAGAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATGAAGCAAACTGCGATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATGAAGCAAACTGCGATGCT	1200
Qy	1201	CAGAAATTCCTAGAAATCTGAAAGATGTTCTGTGATTAACACTTAATACAGATTCACA	1260
Db	1201	CAGAAATTCCTAGAAATCTGAAAGATGTTCTGTGATTAACACTTAATACAGATTCACA	1260
Qy	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAAGTGTAGTCTGTGACTCAGATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAAGTGTAGTCTGTGACTCAGATGATG	1320
Qy	1321	GGGAGTCTGATCAAAATGCCAAAGTAGCTGATGTATGGACGTTCTAAATGAAGTAGATG	1380
Db	1321	GGGAGTCTGATCAAAATGCCAAAGTAGCTGATGTATGGACGTTCTAAATGAAGTAGATG	1380
Qy	1381	AATATCTGCTTCTGAGAGAAATAGACTTACGGCAGAGATCCATGAGGCTTTAA	1440
Db	1381	AATATCTGCTTCTGAGAGAAATAGACTTACGGCAGAGATCCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT	1500
Qy	1501	TTGGGAAAACCTATCGGAGAGGCAAGCCTCCCAACTTAAGCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACCTATCGGAGAGGCAAGCCTCCCAACTTAAGCATGTAACTGAAAATC	1560
Qy	1561	TAATTTATGAGAGATTTGTTACAGAGCACAAGATTAACAAAGGCGTCCCTGCAATA	1620
Db	1561	TAATTTATGAGAGATTTGTTACAGAGCACAAGATTAACAAAGGCGTCCCTGCAATA	1620
Qy	1621	AATTAAGCCTAAAGAGAGACCTACATCAGGCGCTTACCTCGAGATTTATCAAGAAAG	1680
Db	1621	AATTAAGCCTAAAGAGAGACCTACATCAGGCGCTTACCTCGAGATTTATCAAGAAAG	1680
Qy	1681	CAGATTTGCGAGTTCAAAAGAGCTCTGAAATGATTAATCAGGGAATTAACCAAGAGC	1740
Db	1681	CAGATTTGCGAGTTCAAAAGAGCTCTGAAATGATTAATCAGGGAATTAACCAAGAGC	1740
Qy	1741	AGATGGTCAAGTGAATTAATTAATGATGAGTGTGATGAGATTAACCAAGAGTAT	1800
Db	1741	AGATGGTCAAGTGAATTAATTAATGATGAGTGTGATGAGATTAACCAAGAGTAT	1800
Qy	1801	CTATTCAGATGAGAAAAATCCATACCCATATGATCAGTCAAAAAAGAAATCTGTTCA	1860
Db	1801	CTATTCAGATGAGAAAAATCCATACCCATATGATCAGTCAAAAAAGAAATCTGTTCA	1860
Qy	1861	AAAGGAAAGCTGAACCTATTAAGACAGATTAAGCAATATGGAATCTGAAATATCC	1920
Db	1861	AAAGGAAAGCTGAACCTATTAAGACAGATTAAGCAATATGGAATCTGAAATATCC	1920
Qy	1921	ACAATTCAAAAGCACTTAATAAATAATAGCTGAGAGGAAGTCTTCCACAGCATATTC	1980
Db	1921	ACAATTCAAAAGCACTTAATAAATAATAGCTGAGAGGAAGTCTTCCACAGCATATTC	1980
Qy	1981	ATGCGCTTGAACCTAGTAGTACAGTAAGAAATTAAGCCCACTTAATTTGACTGAATTCGAAA	2040
Db	1981	ATGCGCTTGAACCTAGTAGTACAGTAAGAAATTAAGCCCACTTAATTTGACTGAATTCGAAA	2040
Qy	2041	TTGATAGTGTCTTACAGTGAAGAGATTAAGAAAAAGTACACCAATATGCCAGTCA	2100
Db	2041	TTGATAGTGTCTTACAGTGAAGAGATTAAGAAAAAGTACACCAATATGCCAGTCA	2100
Qy	2101	GGCAGACGAGAAACCTTAACAATATGGAAGTAAAGAACTGCACTGAGGCCAAGAGA	2160
Db	2101	GGCAGACGAGAAACCTTAACAATATGGAAGTAAAGAACTGCACTGAGGCCAAGAGA	2160
Qy	2161	GTAAACAGCAAAATGAAGACAGATAAGTAAAGATGACAGAGTACTTCCAGAGCTGA	2220
Db	2161		

Db 2401 AAGATCTGAGAGTAGACGATTTCTTGTACTGCTGCTGATGANTTANGGACTCAGG 2460  
Qy 2461 AAGATCTGCTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACGAACCAATTAAT 2520  
Db 2461 AAGATCTGCTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAGTGTGCAGCATTTGAAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAGTGTGCAGCATTTGAAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580  
Qy 2581 ATATATGAATGACACGAGAGGCTTTAATGATATCCATTGGGACATGAATTAACACAGTC 2640  
Db 2581 ATATATGAATGACACGAGAGGCTTTAATGATATCCATTGGGACATGAATTAACACAGTC 2640  
Qy 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAATGCTGCTAGTATTGTCAGATACAT 2700  
Db 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAATGCTGCTAGTATTGTCAGATACAT 2700  
Qy 2701 TCAGAGTTTCAAAAGCCGCACTATTGCTGTTTCAAAATCCGGAATGCAAGAGAG 2760  
Db 2701 TCAGAGTTTCAAAAGCCGCACTATTGCTGTTTCAAAATCCGGAATGCAAGAGAG 2760  
Qy 2761 AATGTGCAACATTTCTGCCCACCTGCGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCACCTGCGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAAAGAAATATCAAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAAAGAAATATCAAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Qy 2881 AACACATTAATATACCTGCGAGGCTTCCCTGCTGTTGTTGTCAGAAAGATTAAGCAATGATA 2940  
Db 2881 AACACATTAATATACCTGCGAGGCTTCCCTGCTGTTGTTGTTGTCAGAAAGATTAAGCAATGATA 2940  
Qy 2941 ATGCCAAATGATAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Db 2941 ATGCCAAATGATAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Qy 3001 ACGAAACTGAGCTACTTACTCCAAATTAACATGACCTTTTACAAACCCATATGCTATAC 3060  
Db 3001 ACGAAACTGAGCTACTTACTCCAAATTAACATGACCTTTTACAAACCCATATGCTATAC 3060  
Qy 3061 CACCACATTTTCCCATCACTCACTTTGTTTAAATTAATGAGAAATTCCTGTACAGG 3120  
Db 3061 CACCACATTTTCCCATCACTCACTTTGTTTAAATTAATGAGAAATTCCTGTACAGG 3120  
Qy 3121 AAAAATTTGAGAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Db 3121 AAAAATTTGAGAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Qy 3181 GTACAGTGAACACAAATTAGCCGTAAATMACTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAACACAAATTAGCCGTAAATMACTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTGTTCCTCACTAATGAAGGGGCTCCAGATTAATGAAGAA 3300  
Db 3241 CAAGCAATATTAATGAAGTGTTCCTCACTAATGAAGGGGCTCCAGATTAATGAAGAA 3300  
Qy 3301 TAGGTTCCAGTGAAGAAACATTCAGCAGAACTAGGTAGAAAACAGAGGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGAAGAAACATTCAGCAGAACTAGGTAGAAAACAGAGGCAAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGGTCTATAAACAAAGTCTTCTGGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGGTCTATAAACAAAGTCTTCTGGAA 3420  
Qy 3421 GTAATGTAGACATCTGGAATTAATTAATGAAGAAATTAAGAAAGTGTCAAGACTTTA 3480  
Db 3421 GTAATGTAGACATCTGGAATTAATTAATGAAGAAATTAAGAAAGTGTCAAGACTTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTACAGATTAAGTAAACAGGCTTATGGAAGTATGC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTACAGATTAAGTAAACAGGCTTATGGAAGTATGC 3540

Qy 3541 ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTTAGATGATGTAATTAAGG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTTAGATGATGTAATTAAGG 3600  
Qy 3601 AAGATTAAGTATTTGCTGGAATAATGACATTAAGAAAGTCTGCTGTTTACGAAAGG 3660  
Db 3601 AAGATTAAGTATTTGCTGGAATAATGACATTAAGAAAGTCTGCTGTTTACGAAAGG 3660  
Qy 3661 TCCGAAAGGAGAGCTTAGCAGAGTCTCCCTTTCAACCCATACACATTTGGCTCAGG 3720  
Db 3661 TCCGAAAGGAGAGCTTAGCAGAGTCTCCCTTTCAACCCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCCAAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCCAAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTCCAAACATTTGTTATTTGTTAAATTAATTAATTAATTAATTAAT 3840  
Db 3781 AAGAGCTTCCCTGCTCCAAACATTTGTTATTTGTTAAATTAATTAATTAATTAATTAAT 3840  
Qy 3841 CTACTAGGCAATAGCACCGTTGCTACCGAGTGTCTGTAAGAAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCAATAGCACCGTTGCTACCGAGTGTCTGTAAGAAACACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTAAGAAATAGCTTAATTAATGACTGCAATACCAAGGTAATTTGCAAGGATCTC 3960  
Db 3901 TATCATTAAGAAATAGCTTAATTAATGACTGCAATACCAAGGTAATTTGCAAGGATCTC 3960  
Qy 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGTGTGTTTCTTACAGTGA 4020  
Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGTGTGTTTCTTACAGTGA 4020  
Qy 4021 GTGAATTTGAGAGCTTGACTGCAATTAACAACCCAGAGATCTTCTGATTTGTTCTT 4080  
Db 4021 GTGAATTTGAGAGCTTGACTGCAATTAACAACCCAGAGATCTTCTGATTTGTTCTT 4080  
Qy 4081 CCAACCAATGAGGCAATCACTGTAAGCCAGAGGAGTGTGCTGAGTCAAGAAATTTGG 4140  
Db 4081 CCAACCAATGAGGCAATCACTGTAAGCCAGAGGAGTGTGCTGAGTCAAGAAATTTGG 4140  
Qy 4141 TTTGAGATGATGAAGAAAGGAGGAGGCTTGAAGAAATTAATCAAGAAAGGCAACCA 4200  
Db 4141 TTTGAGATGATGAAGAAAGGAGGAGGCTTGAAGAAATTAATCAAGAAAGGCAACCA 4200  
Qy 4201 TGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTGAG 4260  
Db 4201 TGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTGAG 4260  
Qy 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCACTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCACTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATTAACCTGAATGAAGCTCCAGCAGAAATGGCTGAATTAAGCTGTGTAAGAACGC 4380  
Db 4321 AACATTAACCTGAATGAAGCTCCAGCAGAAATGGCTGAATTAAGCTGTGTAAGAACGC 4380  
Qy 4381 ATGGAGCCAGCCTTTCAACAGCTTCCATCAATTAAGTACTTTTCCCTTTGAGG 4440  
Db 4381 ATGGAGCCAGCCTTTCAACAGCTTCCATCAATTAAGTACTTTTCCCTTTGAGG 4440  
Qy 4441 ACCTGGAAATCCAGAACCAAGCAGATCAAGAAAAGCAGTATTAATCTCACAGAAAAGTA 4500  
Db 4441 ACCTGGAAATCCAGAACCAAGCAGATCAAGAAAAGCAGTATTAATCTCACAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTAATGAAGCTCCAGAGGCTTTCTGCTGACAAAGTTGAGGTGTG 4560  
Db 4501 GTGAATACCTTAATGAAGCTCCAGAGGCTTTCTGCTGACAAAGTTGAGGTGTG 4560  
Qy 4561 CAGATAGTTCTACAGTAAATTAAGAAACAGAGAGTGAAGGTCATCCCTTTAAT 4620  
Db 4561 CAGATAGTTCTACAGTAAATTAAGAAACAGAGAGTGAAGGTCATCCCTTTAAT 4620



```

QY 4621 GCCCATCATAGATGATAGTGTGATACATGACAGTGTCTCTGGAGATCTTCAGAAATAGAA 4680
    |||||||
Db 4621 GCCCATCATAGATGATAGTGTGATACATGACAGTGTCTCTGGAGATCTTCAGAAATAGAA 4680
QY 4681 ACTACCATCTCTCAAGAGAGAGAGCTCATTAAAGTTGTGTATGTGAGAGAGCAACAGCTGGAAG 4740
    |||||||
Db 4681 ACTACCATCTCTCAAGAGAGAGAGCTCATTAAAGTTGTGTATGTGAGAGAGCAACAGCTGGAAG 4740
QY 4741 AGTCTGGGCGACACGATTTGTACGGAAACATCTTACTTCCAGAGCAAGATCTAGAGGGA 4800
    |||||||
Db 4741 AGTCTGGGCGACACGATTTGTACGGAAACATCTTACTTCCAGAGCAAGATCTAGAGGGA 4800
QY 4801 CCCCCTACCTGGGATCTGGAATAGGCTCTTCTCTGTATGACCTGTAATCTGATCTTCTG 4860
    |||||||
Db 4801 CCCCCTACCTGGGATCTGGAATAGGCTCTTCTCTGTATGACCTGTAATCTGATCTTCTG 4860
QY 4861 AAGACAGAGCCCCAGAGTGCCTGCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920
    |||||||
Db 4861 AAGACAGAGCCCCAGAGTGCCTGCTGTGGCAACATACCATCTTCAACCTCTGCATTTGA 4920
QY 4921 AAGTTCCTCCCAATTTGAAAGTTGCGAAATCTGCCCCAGAGTCCAGTCTGCTCATACTG 4980
    |||||||
Db 4921 AAGTTCCTCCCAATTTGAAAGTTGCGAAATCTGCCCCAGAGTCCAGTCTGCTCATACTG 4980
QY 4981 ATACTCTGGGTATATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCCAGAAATTGACAG 5040
    |||||||
Db 4981 ATACTCTGGGTATATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCCAGAAATTGACAG 5040
QY 5041 CTTCACAGAGAAAGGTCACAAAGAAATGTCATGGTGGTGTGGGCTGACCCCAAG 5100
    |||||||
Db 5041 CTTCACAGAGAAAGGTCACAAAGAAATGTCATGGTGGTGTGGGCTGACCCCAAG 5100
QY 5101 AATTATGCTGCTGACAAAGTTTGCAGAAACACCAACATCACTTAACTAATCTAATTA 5160
    |||||||
Db 5101 AATTATGCTGCTGACAAAGTTTGCAGAAACACCAACATCACTTAACTAATCTAATTA 5160
QY 5161 CTGAAAGAGCTACTCATGTTGTTATGAAAAACATGCTGAGTTGTTGTGGAACGAGAC 5220
    |||||||
Db 5161 CTGAAAGAGCTACTCATGTTGTTATGAAAAACATGCTGAGTTGTTGTGGAACGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGGTAGTACTTATTTCTGGGTGACC 5280
    |||||||
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGGTAGTACTTATTTCTGGGTGACC 5280
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
    |||||||
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
QY 5341 TCATATGGAAGAAACCAAGGTCACAAAGGAGACAGAAATGCCAGACAGAAATCT 5400
    |||||||
Db 5341 TCATATGGAAGAAACCAAGGTCACAAAGGAGACAGAAATGCCAGACAGAAATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAATG 5460
    |||||||
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAATG 5460
QY 5461 AATGATGATGACAGCTGTGTGTGCTCTGTGTGTAAGAGAGCTTTATCATCTTCACTG 5520
    |||||||
Db 5461 AATGATGATGACAGCTGTGTGTGCTCTGTGTGTAAGAGAGCTTTATCATCTTCACTG 5520
QY 5521 GCACAGAGTGTCCACCAATTTGTTGTTGTGACAGCAATGCTTGGACAGAGACATGGCT 5580
    |||||||
Db 5521 GCACAGAGTGTCCACCAATTTGTTGTTGTGACAGCAATGCTTGGACAGAGACATGGCT 5580
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACACCTGTGGTGAACCCAGAGTGGGTTTGGACA 5640
    |||||||
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACACCTGTGGTGAACCCAGAGTGGGTTTGGACA 5640
QY 5641 GTGTAGCACTCTACGATGCGAGAGAGAGCTGACACTTACCTGATACCCAGATCCCCACA 5700
    |||||||
Db 5641 GTGTAGCACTCTACGATGCGAGAGAGAGCTGACACTTACCTGATACCCAGATCCCCACA 5700
QY 5701 GGCACACTACTGA 5711

```

```

Db 5701 GGCACACTACTGA 5711
    |||||||
RESULT 11
ID T17438 standard; cDNA: 5914 BP.
AC T17438;
DE BRCA1 coding sequence.
KW Cancer therapy: breast and ovarian cancer predisposing gene; immunogen;
KW antibody production; germline alteration; probe; lesion neoplasia; human;
KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
OS Homo sapiens.
FH key Location/Qualifiers
FT cds 120..5711
FT /tag= a
FT /product= BRCA1
PN MO9605306-A2.
PD 22-FEB-1996.
PE 11-AUG-1995; U10202.
PR 12-AUG-1994; US-289221.
PR 02-SEP-1994; US-300266.
PR 16-SEP-1994; US-308104.
PR 29-NOV-1994; US-348824.
PR 24-MAR-1995; US-409305.
PR 07-JUN-1995; US-483553.
PR 07-JUN-1995; US-480784.
PA (MYRI-) MYRIAD GENETICS INC.
PA (CANC-) CANCER INST.
PA (RECH-) CENT RECH DU CHUL.
PI Durocher F, Emi M, Nakamura Y, Simard J, Shattuck-Eidens DM;
DR P-PSDB; R81481.
DR New nucleic acid and polypeptide for mutant or polymorphic BRCA1
PT gene - for diagnosis and therapy of human breast and ovarian cancer
PT and for diagnosing pre-disposition to these cancers
PS Claim 1; Page 119-128; 218pp; English.
CC This sequence represents the cDNA of the human breast and ovarian cancer
CC predisposing gene (BRCA1). Proteins encoded by mutations of this
CC sequence (see T17439-T17453 and T17455-T17529) can be used as immunogens
CC for antibody production. An additional BRCA1 mutant, with a T to G
CC mutation and 59 nucleotide insert (encoding a protein which terminates at
CC residue 75) is also claimed, however the exact location of the mutations
CC is not specified so the sequence could not be created. The mutant BRCA1
CC genes have at least 1 mutation or polymorphism in comparison to this
CC sequence. By detecting a germline alteration in this gene, a
CC predisposition for breast and ovarian cancer can be diagnosed. In one
CC method, BRCA1 mRNA isolated from a tissue sample from a subject has a
CC probe, corresponding to a fragment of this sequence (or an
CC allele-specific probe for a mutation of this sequence), added to it. The
CC conditions allow for hybridisation of the probe to the mRNA, and any
CC hybridisation which occurs is detected. Alternatively, the BRCA1 gene in
CC the tissue sample is isolated, and a shift in electrophoretic mobility of
CC single stranded DNA from the sample on a non-denaturing polyacrylamide
CC gel indicates a mutation. These methods of detection can also diagnose a
CC lesion neoplasia associated with the BRCA1 locus. The methods may be
CC used in gene therapy, protein replacement therapy and protein mimetics,
CC and may be used to screen for drugs in cancer therapy.
SQ Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T;

```

Query Match 100.0%; Score 5709.4; DB 1; Length 5914;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 AGCTGCTAGAGCTCTCTGAGCCCGCACCGAGGCTGTGGGGTTTCTCAGATTAATGGGCC 60
    |||||||
Db 1 AGCTGCTAGAGCTCTCTGAGCCCGCACCGAGGCTGTGGGGTTTCTCAGATTAATGGGCC 60
QY 61 CCTGGCGCTAGAGAGGCGCTTACCCCTCTGCTGGGTAAGTTCAATTTGGAACAGAAAGAAA 120
    |||||||
Db 61 CCTGGCGCTAGAGAGGCGCTTACCCCTCTGCTGGGTAAGTTCAATTTGGAACAGAAAGAAA 120

```



QY 121 TGGATTATCTGCTCTTCGCCGTTGAGAACTACAAAAATGTCATTAATGCTATGACAGAAA 180  
| | | | |  
Db 121 TGGATTATCTGCTCTTCGCCGTTGAGAACTACAAAAATGTCATTAATGCTATGACAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGAACTGCTCCACAAAGGTGACC 240  
| | | | |  
Db 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGAACTGCTCCACAAAGGTGACC 240  
QY 241 ACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACACAGAAAGAGGCGCTTACAGT 300  
| | | | |  
Db 241 ACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACACAGAAAGAGGCGCTTACAGT 300  
QY 301 GTTCCTTTATGTAAGATGATATACCAAAAAGAGCCTTACAGAAAGTACAGATTTAGTC 360  
| | | | |  
Db 301 GTTCCTTTATGTAAGATGATATACCAAAAAGAGCCTTACAGAAAGTACAGATTTAGTC 360  
QY 361 AACCTGTTAGAGAGCTATTGAAAAATCATTTGTGCTTTGAGTTGACAGAGTTTGAGT 420  
| | | | |  
Db 361 AACCTGTTAGAGAGCTATTGAAAAATCATTTGTGCTTTGAGTTGACAGAGTTTGAGT 420  
QY 421 ATGCAAAACAGCTATATATTTTGCAAAAAGGAAATATACCTCTCCGTAACATCTAAAAGATG 480  
| | | | |  
Db 421 ATGCAAAACAGCTATATATTTTGCAAAAAGGAAATATACCTCTCCGTAACATCTAAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGAGGCTACAGAAAACCGTCCAAAAGACTCTACAGAGTG 540  
| | | | |  
Db 481 AAGTTTCTATCATCCAAAGTATGAGGCTACAGAAAACCGTCCAAAAGACTCTACAGAGTG 540  
QY 541 AACCCGAAAAATCTTCCTTCGACAGAAACAGTCTCAGTGTCCAACTCTCAACCTTGAGAA 600  
| | | | |  
Db 541 AACCCGAAAAATCTTCCTTCGACAGAAACAGTCTCAGTGTCCAACTCTCAACCTTGAGAA 600  
QY 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTCTCAAAAGAGTCTGTACATTG 660  
| | | | |  
Db 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTCTCAAAAGAGTCTGTACATTG 660  
QY 661 AATGCGAATCTGATCTTCTGTAAGATACCGTTATATAGGCACTTATTGCAAGTGTGGAG 720  
| | | | |  
Db 661 AATGCGAATCTGATCTTCTGTAAGATACCGTTATATAGGCACTTATTGCAAGTGTGGAG 720  
QY 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGAAACAGGGATGAAATCAGTTTGGATTCTG 780  
| | | | |  
Db 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGAAACAGGGATGAAATCAGTTTGGATTCTG 780  
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGAATGTAACAATACTGAACATCATCAAC 840  
| | | | |  
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGGAATGTAACAATACTGAACATCATCAAC 840  
QY 841 CCAGTAATTAATGATTGTAACACACACTGAGAAACGCTGACCTGAGAGCATCCGAAAAGT 900  
| | | | |  
Db 841 CCAGTAATTAATGATTGTAACACACACTGAGAAACGCTGACCTGAGAGCATCCGAAAAGT 900  
QY 901 ATCAGGAGTGTCTGTTTCAAACTTGCAATGTGAGAGCATGTGGCACAATTACTCATGCCA 960  
| | | | |  
Db 901 ATCAGGAGTGTCTGTTTCAAACTTGCAATGTGAGAGCATGTGGCACAATTACTCATGCCA 960  
QY 961 GCTCATTTACACATGAGAAACAGCACTTTATTACTCACTAAAGCAGAAATGAATGTGAAA 1020  
| | | | |  
Db 961 GCTCATTTACACATGAGAAACAGCACTTTATTACTCACTAAAGCAGAAATGAATGTGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCCTGTGCTTACCAAGAGGCCAACTAACAGAT 1080  
| | | | |  
Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCCTGTGCTTACCAAGAGGCCAACTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGGCGAATCCAGACAGAAAAAGGTAG 1140  
| | | | |  
Db 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGGCGAATCCAGACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAATAGCAAAATGCCATGCT 1200  
| | | | |  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAATAGCAAAATGCCATGCT 1200

QY 1201 CAGAGAAATCCTAGAGATTAAGTAAGATGTTCTTGATTAACACTAAATAGACACTTCAGA 1260  
| | | | |  
Db 1201 CAGAGAAATCCTAGAGATTAAGTAAGATGTTCTTGATTAACACTAAATAGACACTTCAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTTCAGAAAGTGAAGTGAAGTGTAGTGTGATGATGATGATG 1320  
| | | | |  
Db 1261 AAGTTAATGAGTGGTTTTCAGAAAGTGAAGTGAAGTGTAGTGTGATGATGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGATTTGAGACCTTCAATATGAGTAGATG 1380  
| | | | |  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGAATGATTTGAGACCTTCAATATGAGTAGATG 1380  
QY 1381 AATATTCTGCTTCTTACAGAAAAATAGACTTACTGCGCAGTATCCTCATGAGCCTTTAA 1440  
| | | | |  
Db 1381 AATATTCTGCTTCTTACAGAAAAATAGACTTACTGCGCAGTATCCTCATGAGCCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTGAAGTGAATTTGAGCAAAATAT 1500  
| | | | |  
Db 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTGAAGTGAATTTGAGCAAAATAT 1500  
QY 1501 TTGGAAAAACCTATCGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAACATAATC 1560  
| | | | |  
Db 1501 TTGGAAAAACCTATCGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAACATAATC 1560  
QY 1561 TAATTATAGAGCAATTTGTTACTGAGCCACAGATATATACAGAGCGTCCCTCACAAATA 1620  
| | | | |  
Db 1561 TAATTATAGAGCAATTTGTTACTGAGCCACAGATATATACAGAGCGTCCCTCACAAATA 1620  
QY 1621 AATTTAAGGCTTAAAGAGACCTACATCAGGCTTCAATCCTGAGGATTTTATCAAGAAAG 1680  
| | | | |  
Db 1621 AATTTAAGGCTTAAAGAGACCTACATCAGGCTTCAATCCTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAGGGAATCAACCAAGCGAGC 1740  
| | | | |  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAGGGAATCAACCAAGCGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATTAATTAATTAATAGTGTGATGAGATTAATAAAGTGTATT 1800  
| | | | |  
Db 1741 AGAATGCTCAAGTGAATTAATTAATTAATTAATAGTGTGATGAGATTAATAAAGTGTATT 1800  
QY 1801 CTAATTGAGATGAGAAAAATCCTAACCCAAATGATGATCCTGSAAAAAGAAATCTGTTTCA 1860  
| | | | |  
Db 1801 CTAATTGAGATGAGAAAAATCCTAACCCAAATGATGATCCTGSAAAAAGAAATCTGTTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTATTAAGCAGACAGTATTAAGCAATATGGAATCAATTAATATCC 1920  
| | | | |  
Db 1861 AAACGAAAGCTGAACCTATTAAGCAGACAGTATTAAGCAATATGGAATCAATTAATATCC 1920  
QY 1921 ACAATTTCAAAAGCACCTTAATAAAGAAATAGGCTGAGAGGAGTCTTACACAGCATATTC 1980  
| | | | |  
Db 1921 ACAATTTCAAAAGCACCTTAATAAAGAAATAGGCTGAGAGGAGTCTTACACAGCATATTC 1980  
QY 1981 ATGCGCTTGAATTAAGTACGATGAGTAAGTAAAGCCCAATTTGATGTAAGTGAATA 2040  
| | | | |  
Db 1981 ATGCGCTTGAATTAAGTACGATGAGTAAGTAAAGCCCAATTTGATGTAAGTGAATA 2040  
QY 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAATAGCAACCAATATGCACTCA 2100  
| | | | |  
Db 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAATAGCAACCAATATGCACTCA 2100  
QY 2101 GGCACAGCAAAAGCTTACACTCATGGAAGTAAAGAACTGTCAACCTGAGGCCAAGAGA 2160  
| | | | |  
Db 2101 GGCACAGCAAAAGCTTACACTCATGGAAGTAAAGAACTGTCAACCTGAGGCCAAGAGA 2160  
QY 2161 GTTAAAGCAAAATGAAGCAAGTAAGAAAGCAATGACAGGATTAATTTCCACAGCTGA 2220  
| | | | |  
Db 2161 GTTAAAGCAAAATGAAGCAAGTAAGAAAGCAATGACAGGATTAATTTCCACAGCTGA 2220  
QY 2221 AGTTAAACAATGCACTGCTTTTACTAAGTGTCAAAATACCAAGTGAATTAAGAAAT 2280  
| | | | |  
Db 2221 AGTTAAACAATGCACTGCTTTTACTAAGTGTCAAAATACCAAGTGAATTAAGAAAT 2280  
QY 2281 TTGTCAATCTTAGCCTTCCAAAGAGAGAAAAAGAAAGAAACCTAGAAACAGTTAAAGTGT 2340  
| | | | |

Db	2281	TTGTCATTCCTAGCCTTCCAAAGAAAGAAAAAGAAAGAACTAGAAACGTTAAAGCT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAAAGATCTCATGTTAAGTGAAGAAAGGGTTTTCAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAAAGATCTCATGTTAAGTGAAGAAAGGGTTTTCAACTG	2400
Qy	2401	AAACATCTGTAGAGAGTGAAGCATATTTTCATGTGTACCTGGTACTGTTATGCGACTCAGG	2460
Db	2401	AAACATCTGTAGAGAGTGAAGCATATTTTCATGTGTACCTGGTACTGTTATGCGACTCAGG	2460
Qy	2461	AAAGATCTGGTTACTGAGAGTTAGACACTGTAGGAGGCAAAAACAGAACCAATAAT	2520
Db	2461	AAAGATCTGGTTACTGAGAGTTAGACACTGTAGGAGGCAAAAACAGAACCAATAAT	2520
Qy	2521	GTGTAGTCAAGTGTGCAGCATTTTGAAGACCCCAAGGAGCAATTAATCATGGTTTCCAAAG	2580
Db	2521	GTGTAGTCAAGTGTGCAGCATTTTGAAGACCCCAAGGAGCAATTAATCATGGTTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATTCATTTGGGACATGAAGTTAAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATTCATTTGGGACATGAAGTTAAACACAGTC	2640
Qy	2641	GGGAAACAACATRGAATGTGAAGAAAGTGAACCTTATCTCATGTTTGGCAATATAT	2700
Db	2641	GGGAAACAACATRGAATGTGAAGAAAGTGAACCTTATCTCATGTTTGGCAATATAT	2700
Qy	2701	TCAAGTGTTCAAAGCGCCAGCTCATTTTGTCTGTTTCCAATCCAGAAATGCAAGAGAG	2760
Db	2701	TCAAGTGTTCAAAGCGCCAGCTCATTTTGTCTGTTTCCAATCCAGAAATGCAAGAGAG	2760
Qy	2761	AATGTGCAACATTTCTGTGCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGTGCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGGAATGTGAACAAAAGGAAGAAATCAAGAGAAATGAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGGAATGTGAACAAAAGGAAGAAATCAAGAGAAATGAGTCTAATATCAAGCTGTAC	2880
Qy	2881	AGACAGTAAATATACACTGCAGGCTTCTCTGTGGTTGGTCAGAAATATAGCAAGTGTATA	2940
Db	2881	AGACAGTAAATATACACTGCAGGCTTCTCTGTGGTTGGTCAGAAATATAGCAAGTGTATA	2940
Qy	2941	ATGCCAATGTATGATATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAATGTATGATATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Qy	3001	ACGAACTGCACTATTACTCCAAATPAAACATGAGCTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAACTGCACTATTACTCCAAATPAAACATGAGCTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACACATTTTCCCATCAACATCTAATTTGTTAAACTPAAATGTAAAGAAAATCTGCTAGAG	3120
Db	3061	CACACATTTTCCCATCAACATCTAATTTGTTAAACTPAAATGTAAAGAAAATCTGCTAGAG	3120
Qy	3121	AAAACTTTGAGGAACATTCATCTCACTGCGAAAGAAATGGGAATGAGAACTTCCAA	3180
Db	3121	AAAACTTTGAGGAACATTCATCTCACTGCGAAAGAAATGGGAATGAGAACTTCCAA	3180
Qy	3181	GTACAGTGAACCAATTAGCCGTAATPACATTAGAGAAATGTTTTTAAGAGCCAGCT	3240
Db	3181	GTACAGTGAACCAATTAGCCGTAATPACATTAGAGAAATGTTTTTAAGAGCCAGCT	3240
Qy	3241	CAACCATATTATTAAGAGTGTTCACAGTACTPAGTAAGATGGGGCCCGATATTATAGAA	3300
Db	3241	CAACCATATTATTAAGAGTGTTCACAGTACTPAGTAAGATGGGGCCCGATATTATAGAA	3300
Qy	3301	TAGTTCACAGTATGAAGAAACATTCAGACAGAACTAGTGTGAACAACAGAGGCCCAAAATGA	3360
Db	3301	TAGTTCACAGTATGAAGAAACATTCAGACAGAACTAGTGTGAACAACAGAGGCCCAAAATGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTGCACCTGAGGCTATATAACAAAGTCTTCTGTGAA	3420

Dd	3361	ATGTTATGCTTAGATTAGGGGTTTTCGAACTGAGGCTCATTAATAAAGTCTCTCGTGA	3420
Oy	3421	GTAATTGTAGCATCTCTGAAATAAAAAGCAAGATATGAGAGAGTAGTTCAGACTGTTA	3480
Dd	3421	GTAATTGTAGCATCTCTGAAATAAAAAGCAAGATATGAGAGAGTAGTTCAGACTGTTA	3480
Oy	3431	ATACAGATTCTCTCCATATCTGATTTTCAGATTACTTAAGAAGCTTATGGAAATATTC	3540
Dd	3481	ATACAGATTCTCTCCATATCTGATTTTCAGATTACTTAAGAAGCTTATGGAAATATTC	3540
Oy	3541	ATGCATCTCAGGTTTGTCTTGAGACACCGATGAGCTGTAGATCATGSGTGAATAAAGG	3600
Dd	3541	ATGCATCTCAGGTTTGTCTTGAGACACCGATGAGCTGTAGATCATGSGTGAATAAAGG	3600
Oy	3601	AAGATAGTAGTTTGTCTGAAATAGACATTAAAGAAAGTCTGCTCTTTTATAGCAAAACG	3660
Dd	3601	AAGATAGTAGTTTGTCTGAAATAGACATTAAAGAAAGTCTGCTCTTTTATAGCAAAACG	3660
Oy	3661	TCGCAAAAGAGAGACTTACGAGAGATCTTACGCCCTTACCCATACACATTGGCTCAGG	3720
Dd	3661	TCGCAAAAGAGAGACTTACGAGAGATCTTACGCCCTTACCCATACACATTGGCTCAGG	3720
Oy	3721	GTTACCGCAAGGGGGCCAAATAATTAGAGCTTCGACAAAGAACTTATCTAGTGGAGATG	3780
Dd	3721	GTTACCGCAAGGGGGCCAAATAATTAGAGCTTCGACAAAGAACTTATCTAGTGGAGATG	3780
Oy	3781	AAGAGCTCCCTGCTTCCAACTGTTATTTGGTAAATAACAATATACCTTCTCAGT	3840
Dd	3781	AAGAGCTCCCTGCTTCCAACTGTTATTTGGTAAATAACAATATACCTTCTCAGT	3840
Oy	3841	CTACTAGGCATAGCACCGTGTGCTACCGAGTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Dd	3841	CTACTAGGCATAGCACCGTGTGCTACCGAGTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Oy	3901	TATCATTTGAAGAAATAGCTTAAATAGCTGGAGTACACAGGTAATTTGGCAAAAGCATCTC	3960
Dd	3901	TATCATTTGAAGAAATAGCTTAAATAGCTGGAGTACACAGGTAATTTGGCAAAAGCATCTC	3960
Oy	3961	AGGAACATCACCTTAGAGAGAGAAACAAATGTCTGCTAGTGTGTTTCTTCACAGTCA	4020
Dd	3961	AGGAACATCACCTTAGAGAGAGAAACAAATGTCTGCTAGTGTGTTTCTTCACAGTCA	4020
Oy	4021	GTAATTGGAAGACTTGACTGCAATACAAACCCAGAGATCCTTCTTGATGGTCTT	4080
Dd	4021	GTAATTGGAAGACTTGACTGCAATACAAACCCAGAGATCCTTCTTGATGGTCTT	4080
Oy	4081	CCAAACCAATAGAGGCATCACTCTGAAAGCCAGAGGATGCTGAGTACAAAGAAATGG	4140
Dd	4081	CCAAACCAATAGAGGCATCACTCTGAAAGCCAGAGGATGCTGAGTACAAAGAAATGG	4140
Oy	4141	TTTGAGATGATGAAAGAAAGGGAAGGGGCTTGGAGAAATATATACAAAGCAACCA	4200
Dd	4141	TTTGAGATGATGAAAGAAAGGGAAGGGGCTTGGAGAAATATATACAAAGCAACCA	4200
Oy	4201	TGGATTTAAACTTAGGGAAGCAGCATCTGCGGAGTGAGAGTGAACCAAGCGTCTTGAG	4260
Dd	4201	TGGATTTAAACTTAGGGAAGCAGCATCTGCGGAGTGAGAGTGAACCAAGCGTCTTGAG	4260
Oy	4261	ACTGCTCAGGGGCTATCCTCTCAGAGTGAATTTTAAACCTCAGCAGAGAGGATACATATGC	4320
Dd	4261	ACTGCTCAGGGGCTATCCTCTCAGAGTGAATTTTAAACCTCAGCAGAGAGGATACATATGC	4320
Oy	4321	AACATTAACCTGATTAAGCTCCAGCAGGAAATGGCTGAATTAACCTGTGTAGAACGC	4380
Dd	4321	AACATTAACCTGATTAAGCTCCAGCAGGAAATGGCTGAATTAACCTGTGTAGAACGC	4380
Oy	4381	ATGGAGACCCAGCTTCTTACAGCTTACCTTCATATAGTACTCTTCCCTTGAGG	4440
Dd	4381	ATGGAGACCCAGCTTCTTACAGCTTACCTTCATATAGTACTCTTCCCTTGAGG	4440
Oy	4441	ACCTGGAGAAATCCAGAACCAAGACATCTGAGAAAGCAGTATTACTTACAGAGAAAGTA	4500
Dd	4441	ACCTGGAGAAATCCAGAACCAAGACATCTGAGAAAGCAGTATTACTTACAGAGAAAGTA	4500

OY	4501	GGAAATACCCCTATAAGCCACAATTCACAAGGCCCTTTCGCGACAAAGTTTAAAGTGTGCTG	4501
Db	4501	GTCBAATACCTTATTAAGCCAGAAATTCABAAGGCCCTTTCGCTGACAAAGTTTAAAGTGTGCTG	4560
OY	4561	CAGATAGTCTTACCACTAATAAATAAAGAACCCAGAGAGTGGAAAGGTCATCCCTCTTAAT	4620
Db	4561	CAGATAGTCTTACCACTAATAAATAAAGAACCCAGAGAGTGGAAAGGTCATCCCTCTTAAT	4620
OY	4621	GGCCATCATTAAGATGATAGGTGGATGCACATCTGCTCTGGGAGTCCTTACAGATAGAA	4680
Db	4621	GGCCATCATTAAGATGATAGGTGGATGCACATCTGCTCTGGGAGTCCTTACAGATAGAA	4680
OY	4681	ACTACCCATCTCAAGAGAGAGCTCATTTAAGTGTGTGATGTGTGAGAGAGCAACAGCTGGAG	4740
Db	4681	ACTACCCATCTCAAGAGAGAGCTCATTTAAGTGTGTGATGTGTGAGAGAGCAACAGCTGGAG	4740
OY	4741	AGTCTGGGCCACACGATTTTACGGAAACATCTTACTTCCAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTTACGGAAACATCTTACTTCCAGGCAAGATCTAGAGGAA	4800
OY	4801	CCCCCTACCGGAATCGAATCGAATAGCCCTCTCTCTGATGATGCCGAATCTGATCCTCTG	4860
Db	4801	CCCCCTACCGGAATCGAATCGAATAGCCCTCTCTCTGATGATGCCGAATCTGATCCTCTG	4860
OY	4861	AAGACAGAGCCCCAGAGTCACTGCTGTGTGGCAACATACCATCTTCAACCTCTCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCACTGCTGTGTGGCAACATACCATCTTCAACCTCTCATTTGA	4920
OY	4921	AAGTCCCCCAATTGAAAGTTGCGAANAATCCCGCAGATCCACAGCTGCTGCTATCTACTG	4980
Db	4921	AAGTCCCCCAATTGAAAGTTGCGAANAATCCCGCAGATCCACAGCTGCTGCTATCTACTG	4980
OY	4981	ATACCTGCTGGGTAAATGCAATGGAAGAAAGTGTGACAGGAGAGAACCCAGAAATTCAG	5040
Db	4981	ATACCTGCTGGGTAAATGCAATGGAAGAAAGTGTGACAGGAGAGAACCCAGAAATTCAG	5040
OY	5041	CTTCAACACAAAAGGGTCAACAAAAGAATGTCCATGGTGTCTGCGCTGACCCACAGAG	5100
Db	5041	CTTCAACACAAAAGGGTCAACAAAAGAATGTCCATGGTGTCTGCGCTGACCCACAGAG	5100
OY	5101	AATTTATGCTGCTGATCAAGTGTGGCCGAANAACCCACATCACTTAACTAATTAATTA	5160
Db	5101	AATTTATGCTGCTGATCAAGTGTGGCCGAANAACCCACATCACTTAACTAATTAATTA	5160
OY	5161	CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAATTTGTGTGTGAACGAGAC	5220
Db	5161	CTGAAGAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAATTTGTGTGTGAACGAGAC	5220
OY	5221	TGAATATTTTCTAGGAATTTGCGGGAGGAAATGGATAGTACTAATTTCTGGGTGACC	5280
Db	5221	TGAATATTTTCTAGGAATTTGCGGGAGGAAATGGATAGTACTAATTTCTGGGTGACC	5280
OY	5281	AGCTATTTAAAGAAAAGAAAATCTGTAATAGCATGATTTTGAAGTACAGAGAGATGTGG	5340
Db	5281	AGCTATTTAAAGAAAAGAAAATCTGTAATAGCATGATTTTGAAGTACAGAGAGATGTGG	5340
OY	5341	TCAATGGAAGAAACCAACAGGTCCAAAGCGACCAAGAGAAATCCACAGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACAGGTCCAAAGCGACCAAGAGAAATCCACAGACAGAAAGATCT	5400
OY	5401	TCAGGAGGGCTAGAAATCTGTGTATGTGGGCCCTTCCACCAATAGCCCAAGATCAATG	5460
Db	5401	TCAGGAGGGCTAGAAATCTGTGTATGTGGGCCCTTCCACCAATAGCCCAAGATCAATG	5460
OY	5461	AATGATGCTACAGCTGTGTGTGCTTCTGTGTGTGAAGAGCTTCTCATCTACACCTTG	5520
Db	5461	AATGATGCTACAGCTGTGTGTGCTTCTGTGTGTGAAGAGCTTCTCATCTACACCTTG	5520
OY	5521	GCACAGGTGTCCACCAATTTGTGTGTGTGACAGCCAGATGCTGTGACAGAGACAAATGCT	5580
Db	5521	GCACAGGTGTCCACCAATTTGTGTGTGTGTGACAGCCAGATGCTGTGACAGAGACAAATGCT	5580

YQ	5581	TCGATGCAATTTGGGACAGTGTGAGACACCTGTGTGACCCGAGAGTGGGTGGACA	5640
Db	5581	TCGATGCAATTTGGGACAGTGTGAGACACCTGTGTGACCCGAGAGTGGGTGGACA	5640
YQ	5641	GTATGACACTTACCAAGTGCAGAGCTGAGACACCTACTGTATACCCAGATCCGCCACA	5700
Db	5641	GTATGACACTTACCAAGTGCAGAGCTGAGACACCTACTGTATACCCAGATCCGCCACA	5700
YQ	5701	GGCACTACTGA	5711
Db	5701	GGCACTACTGA	5711
RESULT 12			
ID	T32601	standard; cDNA; 5914 BP.	
AC	T32601;		
DE	BRCA1, breast and ovarian cancer susceptibility gene.		
KW	BRCA1; breast cancer; ovary cancer; predisposing gene; diagnosis;		
OS	susceptibility gene; prognosis; gene therapy; ds.		
FM	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	cds	120..5711	
FT		/*tag-a	
FT		/product= BRCA1 protein	
PN	MO605308-A1.		
PD	22-FEB-1996.		
PF	11-AUG-1995; U10220.		
PR	12-AUG-1994; US-289221.		
PR	02-SEP-1994; US-300266.		
PR	16-SEP-1994; US-308104.		
PR	29-NOV-1994; US-348824.		
PR	24-MAR-1995; US-409305.		
PR	07-JUN-1995; US-488011.		
PR	07-JUN-1995; US-483554.		
PR	07-JUN-1995; US-487002.		
PA	(MRT-) MTRAD GENETICS INC.		
PA	(UTAH) UNIV UTAH RES FOUND.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PI	Futreal PA, Goldgar DE, Harsman KD, Kamb A, Miki Y;		
PI	Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;		
PI	Wieman RM;		
PI	Wpr: 96-139704/14.		
DR	P-FSDB; R97128.		
PT	New method for diagnosing a predisposition to breast and ovarian		
PT	cancer - by detecting a germline alteration in the BRCA1 gene or		
PT	gene regulatory sequence; for gene therapy and to screen for drugs		
PS	Claim 4; Page 108-117; 200pp: English.		
CC	This is the nucleotide sequence of the breast and ovarian cancer		
CC	susceptibility gene, BRCA1. Four kindred families provided genetic		
CC	evidence for localisation of BRCA1 to a sufficiently small region for		
CC	the application of positional cloning strategies. A detailed map of		
CC	transcripts was developed for the region of 17q21 between D17S1321 and		
CC	D17S1224. A combination of sequences obtd. from cDNA clones,		
CC	hybrid-selected sequences and PCR prods. allowed construction of a		
CC	composite full-length BRCA1 cDNA (see J32612 for genomic sequence).		
CC	The isolated cDNA is used in methods for either diagnosis of the		
CC	predisposition to cancer (partic. breast and ovarian cancer), or for the		
CC	diagnosis or prognosis of cancer, and also in gene-based therapies		
CC	directed at cancer cells.		
SQ	Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T;		
Query Match 100.0%; Score 5709.4; DB 1; Length 5914;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
YQ	1	AGCGCGCTGAGACTTCTCTGAGCCCGGACAGCGTGGGCTTCAGATTAACGGGCC	60
Db	1	AGCGCGCTGAGACTTCTCTGAGCCCGGACAGCGTGGGCTTCAGATTAACGGGCC	60
YQ	61	CTGCGCTCAGAGGCGCTTACCTCTGTGCTGGGTAAAGTTCATTGAGACACAAAGAAA	120

Db	61	CTGCGCTCAGGAGGCGCTTCAACCTCTGCTTGGTAAAGTTCAATTGAAACGAAAGAAA	120
Oy	121	TGATTTATTCGTGCTCTCCGGGTGAAGAAATACAAATGTCAATTATGCTATGACGAAAA	180
Db	121	TGATTTATTCGTGCTCTCCGGGTGAAGAAATACAAATGTCAATTATGCTATGACGAAAA	180
Oy	181	TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC	240
Db	181	TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC	240
Oy	241	ACATATTTTGCATTTTGGATGCTGAAACTTCTCAACCAAGAAAGAGGCGCTTACAGT	300
Db	241	ACATATTTTGCATTTTGGATGCTGAAACTTCTCAACCAAGAAAGAGGCGCTTACAGT	300
Oy	301	GTCCCTTATGTAAAGATATATAACCAAAAGAGCCTACAAAGAAAGTACGATTTATCTC	360
Db	301	GTCCCTTATGTAAAGATATATAACCAAAAGAGCCTACAAAGAAAGTACGATTTATCTC	360
Oy	361	AACTTGTGAAGAGCTATGTGAAAATCATTTTGTCTTTACGTTTGACACAGGTTGGAGT	420
Db	361	AACTTGTGAAGAGCTATGTGAAAATCATTTTGTCTTTACGTTTGACACAGGTTGGAGT	420
Oy	421	ATGCAACAGCTATATTTTGCAAAAAAGGAAATATACCTCTGTGAAACATCTAAAAAGATG	480
Db	421	ATGCAACAGCTATATATTTTGCAAAAAAGGAAATATACCTCTGTGAAACATCTAAAAAGATG	480
Oy	481	AAAGTTTCATCATCAAGATATGGGCTACAGAAACCGTGCACAAAAGACTTCTACAGAGTG	540
Db	481	AAAGTTTCATCATCAAGATATGGGCTACAGAAACCGTGCACAAAAGACTTCTACAGAGTG	540
Oy	541	AAACCCGAAAATCTCTCTGTCAGAGAAACCAAGTCAAGTGTCCAACTCTCTAACCTTGGAA	600
Db	541	AAACCCGAAAATCTCTCTGTCAGAGAAACCAAGTGTCCAACTCTCTAACCTTGGAA	600
Oy	601	CTGTGAAACCTCTAGAGCAACAGCAGGGAATACAACTCAAAAGAGCTGTCTACATTG	660
Db	601	CTGTGAAACCTCTAGAGCAACAGCAGGGAATACAACTCAAAAGAGCTGTCTACATTG	660
Oy	661	AATGGGATCTGATCTCTTCGAAGATACCGTATATAGGAACCTATTGCACTGTGGAG	720
Db	661	AATGGGATCTGATCTCTTCGAAGATACCGTATATAGGAACCTATTGCACTGTGGAG	720
Oy	721	ATCAAGAATTTGTTCAAAATCACCCCTCAAGAACCAAGGATGAATCACTTTGGATTCTG	780
Db	721	ATCAAGAATTTGTTCAAAATCACCCCTCAAGAACCAAGGATGAATCACTTTGGATTCTG	780
Oy	781	CAAAAAAGGCTGCTTGTGCAATTTTCTGAGCGGATTAACAATCTGACATCATCTAAC	840
Db	781	CAAAAAAGGCTGCTTGTGCAATTTTCTGAGCGGATTAACAATCTGACATCATCTAAC	840
Oy	841	CCAGATTAATGATTTTGAACCAACCACTGAGAGGCTCAGCTGAGAGCAATCCAGAAAGT	900
Db	841	CCAGATTAATGATTTTGAACCAACCACTGAGAGGCTCAGCTGAGAGCAATCCAGAAAGT	900
Oy	901	ATCAGGAGTAGTTCTGTTTCAACCTGCGATGTGAGCCATGTGGCACAAAATACTCATGCCA	960
Db	901	ATCAGGAGTAGTTCTGTTTCAACCTGCGATGTGAGCCATGTGGCACAAAATACTCATGCCA	960
Oy	961	GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGCAAGATGATGTAGAAA	1020
Db	961	GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGCAAGATGATGTAGAAA	1020
Oy	1021	AGGCGAATTTCTGTAAATTAAGCAACAGCCTGGCTTACCAAGAGCCCAACATTAACAAT	1080
Db	1021	AGGCGAATTTCTGTAAATTAAGCAACAGCCTGGCTTACCAAGAGCCCAACATTAACAAT	1080
Oy	1081	GGGCTGGAAGTAAAGAAACAATGTATGATAGGGGAGCTCCACAGACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAAACAATGTATGATAGGGGAGCTCCACAGACAGAAAAAAGGTAG	1140
Oy	1141	ATCTGAATGCTGATCCCTGTGTGAGAAAGAAATGAAATAGCAAGAACTGCCATGCT	1200

Dd	1141	ATTCGAATGCTGATCCCTCTGTGTGAAGAAAAGAAATGGAATAGACGAAGAACTGCATGCT	1200
Qy	1201	CAGAAATCCTAGAGATACTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA	1260
Dd	1201	CAGAGAAATCCTAGAGATACTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA	1260
Qy	1261	AAAGTTAATGAGTGGTTTTCCAGAAAGTATGAACGTGTAGGTTCTGATGACTCATATGATG	1320
Dd	1261	AAAGTTAATGAGTGGTTTTCCAGAAAGTATGAACGTGTAGGTTCTGATGACTCATATGATG	1320
Qy	1321	GGGAGTCGMAATCAAAAGCCAAAGTATGCTGATGTATGGAGCTTCTAAATGAGTATGATG	1380
Dd	1321	GGGAGTCGMAATCAAAAGCCAAAGTATGCTGATGTATGGAGCTTCTAAATGAGTATGATG	1380
Qy	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTGGCCAGTATCCTATGAGGCTTTAA	1440
Dd	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTGGCCAGTATCCTATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGGTTCACTCCAAATCAGTAGAGAGTAAATTGAGACAAATAT	1500
Dd	1441	TATGTAAAGTGAAGAGGTTCACTCCAAATCAGTAGAGAGTAAATTGAGACAAATAT	1500
Qy	1501	TTGGGAAAACCTATCGGAAAGAGCAAGGCTCCCAACTAAGCCATGAACTGAAAATC	1560
Dd	1501	TTGGGAAAACCTATCGGAAAGAGCAAGGCTCCCAACTAAGCCATGAACTGAAAATC	1560
Qy	1561	TAAATATAGAGAGCATTTGTTACTAGACCACAGATTAATACAAAGGCTCCCTCACAAATA	1620
Dd	1561	TAAATATAGAGAGCATTTGTTACTAGACCACAGATTAATACAAAGGCTCCCTCACAAATA	1620
Qy	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG	1680
Dd	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAABACCTCGTAAATGATTAATAGGGAACTAAACAAAGGAGC	1740
Dd	1681	CAGATTTGGCAGTTCAAAABACCTCGTAAATGATTAATAGGGAACTAAACAAAGGAGC	1740
Qy	1741	AGAAATGCTCAAGTATGAATTTACTAATATAGTGTGATGAGATTAACAAAGGTCAT	1800
Dd	1741	AGAAATGCTCAAGTATGAATTTACTAATATAGTGTGATGAGATTAACAAAGGTCAT	1800
Qy	1801	CTATTCAGAAATGAGAAAAATCCTAACCCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA	1860
Dd	1801	CTATTCAGAAATGAGAAAAATCCTAACCCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA	1860
Qy	1861	AAAGGAAAGCTGAACCTATAAGCAGAGATATAAGCAATATGGAATCTCGAATTTAAATATCC	1920
Dd	1861	AAAGGAAAGCTGAACCTATAAGCAGAGATATAAGCAATATGGAATCTCGAATTTAAATATCC	1920
Qy	1921	ACAATTCAAAAAGCACCTTAATAAAGATAGGCTGGAGAGAGCTTCTTACCGAGCATATTC	1980
Dd	1921	ACAATTCAAAAAGCACCTTAATAAAGATAGGCTGGAGAGAGCTTCTTACCGAGCATATTC	1980
Qy	1981	ATGGCTTGAACATAGTAGTCAGTAGAAATCTAAGCCCACTAATTTGACTGATGTCGAAA	2040
Dd	1981	ATGGCTTGAACATAGTAGTCAGTAGAAATCTAAGCCCACTAATTTGACTGATGTCGAAA	2040
Qy	2041	TTGATAGTGTGTTCTAGCAGTAGGAAGACATTAAGAAAAAAAAGTACAAACAAATGCCAGTCA	2100
Dd	2041	TTGATAGTGTGTTCTAGCAGTAGGAAGACATTAAGAAAAAAAAGTACAAACAAATGCCAGTCA	2100
Qy	2101	GGCAGACAGAAACCTACACATCATGGAAGGTAAAGACCTGCAACTGGAGCCAAAGAA	2160
Dd	2101	GGCAGACAGAAACCTACACATCATGGAAGGTAAAGACCTGCAACTGGAGCCAAAGAA	2160
Qy	2161	GTAACAAGCCAAATGAAACACACAGTAAAGAAAGACATGACAGCATCTTCCAGAGCTGA	2220
Dd	2161	GTAACAAGCCAAATGAAACACACAGTAAAGAAAGACATGACAGCATCTTCCAGAGCTGA	2220
Qy	2221	AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTAGAACTTAAAGAT	2280
Dd	2221	AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTAGAACTTAAAGAT	2280

QY	2281	TTTCTCAATCCTACCTTCCAGAGAGAGAAAAAGAGAAACCTAGAAACAGTTAAAGT	2340
Db	2281	TTGTCAATCCTACCTTCCAGAGAGAGAAAAAGAGAAACCTAGAAACAGTTAAAGT	2340
QY	2341	CTAATATGCTGAGAGCCCAAGATGCTCATGTATAGTGGAGAAAGGTTTTGCCAACTG	2400
Db	2341	CTAATATGCTGAGAGCCCAAGATGCTCATGTATAGTGGAGAAAGGTTTTGCCAACTG	2400
QY	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCATTTGCTGCTGCTGCTAGTATATGGCACTCAG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCATTTGCTGCTGCTGCTAGTATATGGCACTCAG	2460
QY	2461	AAAGTATCTGTTACTGGAAGTTAGCCTGTAGGAGAGGCAAAAACGAACCAATTAAT	2520
Db	2461	AAAGTATCTGTTACTGGAAGTTAGCCTGTAGGAGAGGCAAAAACGAACCAATTAAT	2520
QY	2521	GTGTGAGTCAGTGTGCAGCATTTTGAAAAACCCCAAGGGACTAATTCATGTTGTTCAAAG	2580
Db	2521	GTGTGAGTCAGTGTGCAGCATTTTGAAAAACCCCAAGGGACTAATTCATGTTGTTCAAAG	2580
QY	2581	ATPATGGAATGACACAGAGGCTTTAAAGTATTCATTGGGACATGAAGTTAACCAAGTC	2640
Db	2581	ATPATGGAATGACACAGAGGCTTTAAAGTATTCATTGGGACATGAAGTTAACCAAGTC	2640
QY	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGCAGATATCAT	2700
Db	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGCAGATATCAT	2700
QY	2701	TCAGGTTTCAAAAGGCCAGCTATTGCTCTGTTTTCAATCCAGAAATGACAGAAAGG	2760
Db	2701	TCAGGTTTCAAAAGGCCAGCTATTGCTCTGTTTTCAATCCAGAAATGACAGAAAGG	2760
QY	2761	AATGTCAACATCTCTGCCCACCTCGGGGCTTAAAGAAACAAGTCCAAAGTCACT	2820
Db	2761	AATGTCAACATCTCTGCCCACCTCGGGGCTTAAAGAAACAAGTCCAAAGTCACT	2820
QY	2821	TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGATGAGTAAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGATGAGTAAATATCAAGCTGTAC	2880
QY	2881	AACAGGTTAATATCACTGCGAGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881	AACAGGTTAATATCACTGCGAGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
QY	2941	ATGCCAATATGATATCAAGAGAGGCTCATGATTTTGTCTATCATCTCAAGTTCAGAGCA	3000
Db	2941	ATGCCAATATGATATCAAGAGAGGCTCATGATTTTGTCTATCATCTCAAGTTCAGAGCA	3000
QY	3001	ACGAACCTGGACTCATTTACTCCAAATTAACATGGACTTTTACAAAACCCATATCGATAC	3060
Db	3001	ACGAACCTGGACTCATTTACTCCAAATTAACATGGACTTTTACAAAACCCATATCGATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATTAAGAAAAAATCTGTGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATTAAGAAAAAATCTGTGAGG	3120
QY	3121	AAAACCTTGAGGACATTTCAATGTCACTGTGAAAGAGAAATGGGAAATGAGACATTTCCA	3180
Db	3121	AAAACCTTGAGGACATTTCAATGTCACTGTGAAAGAGAAATGGGAAATGAGACATTTCCA	3180
QY	3181	GTACAGTGACAAATTTACCCGTAATTAACATTGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
Db	3181	GTACAGTGACAAATTTACCCGTAATTAACATTGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
QY	3241	CAAGCAATTTATGAAGTAGTTCAGTACTAATGAAGGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATTTATGAAGTAGTTCAGTACTAATGAAGGGGCTCCAGTATTAATGAAA	3300
QY	3301	TAGGTTCCAGTATGAAGAAATTCAGACAGAACTAGGTAGAAACAGAGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAGAAATTCAGACAGAACTAGGTAGAAACAGAGGCCAAATTTGA	3360

QY	3361	ATGCGATCGTTAAGATTAAGGGGTTTGGACCTGAGGCTAATAACAAAGCTCTCCGTGAA	3420
Db	3361	ATGCGATCGTTAAGATTAAGGGGTTTGGACCTGAGGCTAATAACAAAGCTCTCCGTGAA	3420
QY	3421	GTAATTGTAGCATCCCTGAAATATAAAAAGCAAGAAATATGAAGAGTACTGACACTGTTA	3480
Db	3421	GTAATTGTAGCATCCCTGAAATATAAAAAGCAAGAAATATGAAGAGTACTGACACTGTTA	3480
QY	3481	ATACGATTTTCTTCOCATATCTGATTTCAATATTAACACAGCCTATGGAGTAGTC	3540
Db	3481	ATACGATTTTCTTCOCATATCTGATTTCAATATTAACACAGCCTATGGAGTAGTC	3540
QY	3541	ATGCATCTCAGGTTGGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATTAAGG	3600
QY	3601	AAGATCTAGTGTTCGTAATAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACCG	3660
Db	3601	AAGATCTAGTGTTCGTAATAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACCG	3660
QY	3661	TCCCAAAAGGAGAGCTTAGACAGAGGAGTCTGAGCCTTCAACCATATGAGTTGGCTCAGG	3720
Db	3661	TCCCAAAAGGAGAGCTTAGACAGAGGAGTCTGAGCCTTCAACCATATGAGTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAGAGAACTTATCTAGTGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAGAGAACTTATCTAGTGAGATG	3780
QY	3781	AAGAGCTCCCTGCTTCCACACCTGTGATTTGGTAAATGAACAATATACCTTTCAGT	3840
Db	3781	AAGAGCTCCCTGCTTCCACACCTGTGATTTGGTAAATGAACAATATACCTTTCAGT	3840
QY	3841	CTACTAGGCATAGACACCGTTGCTACGAGTGTGTGCTTAAGAACACAGAGAGAAATTAT	3900
Db	3841	CTACTAGGCATAGACACCGTTGCTACGAGTGTGTGCTTAAGAACACAGAGAGAAATTAT	3900
QY	3901	TATCATTTGAGATAGCTTAATATGACTGCATACACGTAATATTGGCAAGAGCATATC	3960
Db	3901	TATCATTTGAGATAGCTTAATATGACTGCATACACGTAATATTGGCAAGAGCATATC	3960
QY	3961	AGGAACATCACCTTAGAGSAGSAAACAAATGTCTGCTGAGCTGTTTCTTCACAGTSCA	4020
Db	3961	AGGAACATCACCTTAGAGSAGSAAACAAATGTCTGCTGAGCTGTTTCTTCACAGTSCA	4020
QY	4021	GTCGATTTGGAAGACTTACTGTCGAAATACAAACCCAGAGATCCTTCTGATTTGGTCTT	4080
Db	4021	GTCGATTTGGAAGACTTACTGTCGAAATACAAACCCAGAGATCCTTCTGATTTGGTCTT	4080
QY	4081	CCAAACAAATGAGGCATCACTGTGAAAGCCAGGAGATTTGCTGTGAGTACACAGAAATTGG	4140
Db	4081	CCAAACAAATGAGGCATCACTGTGAAAGCCAGGAGATTTGCTGTGAGTACACAGAAATTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGAACGCGGCTTGGAAAGAAATATATACAAAGACAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAACGCGGCTTGGAAAGAAATATATACAAAGACAAAGCA	4200
QY	4201	TGGATTCAAACTTAGTGTGAAGACGACATCTGGGTGTGAGAGTAAACAAAGCTTCTGAG	4260
Db	4201	TGGATTCAAACTTAGTGTGAAGACGACATCTGGGTGTGAGAGTAAACAAAGCTTCTGAG	4260
QY	4261	ACTGCTCAGGGCTTCTCTCCACAGAGTGAACATTTTAACCTCAGCAGAGGGATACATGC	4320
Db	4261	ACTGCTCAGGGCTTCTCTCCACAGAGTGAACATTTTAACCTCAGCAGAGGGATACATGC	4320
QY	4321	AACATTAACCTGATTAAGCTTCACAGCAGAGAAATGGCTGAACCTAGAACCTGTGTAGAACGC	4380
Db	4321	AACATTAACCTGATTAAGCTTCACAGCAGAGAAATGGCTGAACCTAGAACCTGTGTAGAACGC	4380
QY	4381	ATGGGAGCCAGCCTTCTAACAAGTACCCTTCCATCATTAAGTACATCTTCTGCTTGAG	4440
Db	4381	ATGGGAGCCAGCCTTCTAACAAGTACCCTTCCATCATTAAGTACATCTTCTGCTTGAG	4440
QY	4441	ACCTGCGAAATCCAGAAACAAGACATCTCAGAAAGAGAGTATTAACTTCACAGAAAGTA	4500

```

Db 4441 ACCGGAATCCAGACAAAGACATCAGAAAAACAGATTAACTTCAGAAAAAGTA 4500
Qy 4501 GTGAATACCCATATAGCCAGAAATCCAGAGGCCCTTCTGCTGCAAGTTTGAGTGTCTG 4560
Db 4501 GTGAATACCCATATAGCCAGAAATCCAGAGGCCCTTCTGCTGCAAGTTTGAGTGTCTG 4560
Qy 4561 CAGATAGTTCTTACAGTAAAAAATAAAGAACAGAGAGTGGAAAGTATCCCTTCTTAAT 4620
Db 4561 CAGATAGTTCTTACAGTAAAAAATAAAGAACAGAGAGTGGAAAGTATCCCTTCTTAAT 4620
Qy 4621 GCCCATCATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
Db 4621 GCCCATCATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
Qy 4681 ACTACCATCTCTAAGAGAGAGCTCATTAAGTTGTTGATGATGATGATGATGATGATGATGAT 4740
Db 4681 ACTACCATCTCTAAGAGAGAGCTCATTAAGTTGTTGATGATGATGATGATGATGATGATGAT 4740
Qy 4741 AGTCTGGCCACACGATTTGAGGAAAAATCTTACTTGCACAGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGCCACACGATTTGAGGAAAAATCTTACTTGCACAGCAAGATCTAGAGGAA 4800
Qy 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTCTGATGATGATGATGATGATGATGATGATGAT 4860
Db 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTCTGATGATGATGATGATGATGATGATGATGAT 4860
Qy 4861 AAGACAGAGAGAGAGAGAGTCTGTTGGCAACATACATCTTCAACCTCTGATGATGATGAT 4920
Db 4861 AAGACAGAGAGAGAGAGAGTCTGTTGGCAACATACATCTTCAACCTCTGATGATGATGATGAT 4920
Qy 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGTCTGCTCATACTACTG 4980
Db 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGTCTGCTCATACTACTG 4980
Qy 4981 ATACTCTGGGTATATGGAATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5040
Db 4981 ATACTCTGGGTATATGGAATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5040
Qy 5041 CTTCACAGAGAGAGTCAACAAAGATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 5100
Db 5041 CTTCACAGAGAGAGTCAACAAAGATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 5100
Qy 5101 AATTATGCTCGTGTACAAAGTTGCCAGAAAACACCAATCACTTAATCTAATTA 5160
Db 5101 AATTATGCTCGTGTACAAAGTTGCCAGAAAACACCAATCACTTAATCTAATTA 5160
Qy 5161 CTGAAGAGAGTCTCTATGTTGTTATGAAACAGATGATGATGATGATGATGATGATGATGATGAT 5220
Db 5161 CTGAAGAGAGTCTCTATGTTGTTATGAAACAGATGATGATGATGATGATGATGATGATGATGAT 5220
Qy 5221 TGAATATTTTCTAGGAATTTGGGAGGAAAAATGGTAGTACTTATTTCTGGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATTTGGGAGGAAAAATGGTAGTACTTATTTCTGGGTGACCC 5280
Qy 5281 AGCTATTTAAAGAAAAAATGCTGAATGAGCATGATTTTGAAGCAAGAGGAGATGTGG 5340
Db 5281 AGCTATTTAAAGAAAAAATGCTGAATGAGCATGATTTTGAAGCAAGAGGAGATGTGG 5340
Qy 5341 TCAATGAGAGAAACCAAGAGGCAAGAGGCAAGAGCAAGAAATCCCGAGCAAGAAATCT 5400
Db 5341 TCAATGAGAGAAACCAAGAGGCAAGAGGCAAGAGCAAGAAATCCCGAGCAAGAAATCT 5400
Qy 5401 TCAGGGGCTAGAAATCTGTGCTATGAGGCCCTTCAACAATGCCCAAGATCAACTGG 5460
Db 5401 TCAGGGGCTAGAAATCTGTGCTATGAGGCCCTTCAACAATGCCCAAGATCAACTGG 5460
Qy 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520
Qy 5521 GCACAGGTGCCCAATTTGTTGTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580
Db 5521 GCACAGGTGCCCAATTTGTTGTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580

```

```

Db 5521 GCACAGGTGCCCAATTTGTTGTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580
Qy 5581 TCCATGCAATTTGGGAGAGATGATGAGGACCTGTGTGACCCGAGAGTGGTGTGGACA 5640
Db 5581 TCCATGCAATTTGGGAGAGATGATGAGGACCTGTGTGACCCGAGAGTGGTGTGGACA 5640
Qy 5641 GTGTAGCACTTACCAAGTCCAGAGAGCTGAGACCTACTGATACCAGATCCCCCA 5700
Db 5641 GTGTAGCACTTACCAAGTCCAGAGAGCTGAGACCTACTGATACCAGATCCCCCA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 13
T84840
ID T84840 standard; cDNA to mRNA; 5712 BP.
AC T84840; 1998 (first entry)
DE Human breast and ovarian cancer susceptibility gene BRCA1.
KW BRCA1; breast cancer; ovarian cancer; human;
KW tumour suppressor gene; gene therapy; receptor; ds.
OS Homo sapiens.
FH Key
FT CDS Location/Qualifiers
FT a
FT /transl_except- (pos:1482..1484, aa:Asp)
FT /transl_except- (pos:1581..1583, aa:Ser)
FT /transl_except- (pos:1889..1901, aa:Glu)
FT /transl_except- (pos:1902..1904, aa:Leu)
FT /transl_except- (pos:1905..1907, aa:Glu)
FT /transl_except- (pos:1908..1910, aa:Leu)
FT /transl_except- (pos:1911..1913, aa:Asn)
FT /transl_except- (pos:1914..1916, aa:Ile)
FT /transl_except- (pos:1917..1919, aa:Met)
FT /transl_except- (pos:4476..4478, aa:Val)
FT /transl_except- (pos:4476..4478, aa:Val)
FT /transl_except- (pos:4479..4481, aa:Val)
FT /transl_except- (pos:4482..4484, aa:Gln)
FT /transl_except- (pos:4689..4691, aa:Pro)

MO9730108-A1.
PD 21-AUG-1997.
PF 19-FEB-1997; U03340.
PR 20-FEB-1996; US-603753.
PA (UYVA-) UNIV VANDERBILT.
PA (UNIM) UNIV WASHINGTON.
PI Claire-King M, Holt JT, Jensen RA, Jetton TL, Page DL,
PI Robinson-Benton CL, Szabo CI, Thompson ME;
DR P-PsDB; W23286.
DR BRCA1 and BRCA2 tumour suppressor gene products - useful to inhibit
PT breast and ovarian cancer cell growth and tumorigenesis, or treat
PT gene linked hereditary or sporadic ovarian or breast cancer
PS Clam 13; Page 34-63; 148bp; English.
CC This sequence comprises a full-length BRCA1 cDNA. Genetic analysis
CC of familial and ovarian cancer indicates that BRCA1 is a tumour
CC suppressor gene. It encodes a 190 kDa protein (see W23286) that is
CC an inhibitor of the growth and proliferation of human breast and
CC ovarian cancer cells. DNA encoding the BRCA1 protein can thus be
CC used in gene therapy methods for the treatment of breast and
CC ovarian cancers. A purified BRCA1 protein can also be used to treat
CC these cancers and, since it is secreted, can be used to identify
CC the BRCA1 receptor and hence to identify BRCA1 protein-mimetic
CC agents which act on the receptor for use in breast and ovarian
CC cancer treatment. The BRCA2 gene (see T84411) and BRCA2 protein
CC (see W23287) have also been characterised. Methods are claimed for
CC the isolation of BRCA1 or BRCA2 receptors, and for treating or
CC preventing breast and (gene-linked hereditary or sporadic) ovarian
CC cancers using BRCA1 and BRCA2 proteins and genes.
SQ Sequence 5712 BP; 1956 A; 1099 C; 1274 G; 1383 T;

```



Query Match		100.0%	Score 5709.4	DB 1	Length 5712
Best Local Similarity		100.0%	Pred. No. 0		
Matches 5710: Conservative		0	Mismatches 1	Indels 0	Gaps 0
QY	1	AGCTGCTGAGACTTCTCTGACCCCGACCCGACGCTGCGGCTTTCAGATTAAGTGGCC	60		
Db	1	AGCTGCTGAGACTTCTCTGACCCCGACCCGACGCTGCGGCTTTCAGATTAAGTGGCC	60		
QY	61	CCTGCGCTCAGAGAGCCCTTACCCCTGCTGCTGGGTAAAGTTGATGGAAACAGAAAGAA	120		
Db	61	CCTGCGCTCAGAGAGCCCTTACCCCTGCTGCTGGGTAAAGTTGATGGAAACAGAAAGAA	120		
QY	121	TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATCCAGAAAA	180		
Db	121	TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATCCAGAAAA	180		
QY	181	TCTTAGAGTGTCCACTCTCTGAGAGTTGATCAAGAACCTGTCTCCACAAAGTGTACC	240		
Db	181	TCTTAGAGTGTCCACTCTCTGAGAGTTGATCAAGAACCTGTCTCCACAAAGTGTACC	240		
QY	241	ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCCCTTCAAGT	300		
Db	241	ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCCCTTCAAGT	300		
QY	301	GTCCTTATGTAGAATGATATACCAAAAGAGCCTACAGAAAGTACAGATTTAGTC	360		
Db	301	GTCCTTATGTAGAATGATATACCAAAAGAGCCTACAGAAAGTACAGATTTAGTC	360		
QY	361	AACTGTGTAAGAGCTATTTGAAATCATTTGTGCTTTTCAAGTTGACAGAGTTGAGT	420		
Db	361	AACTGTGTAAGAGCTATTTGAAATCATTTGTGCTTTTCAAGTTGACAGAGTTGAGT	420		
QY	421	ATGCAAAACGCTATATTTTGCAGAAAAAGAAATTAATCTCTGTAACCTTAAAGATG	480		
Db	421	ATGCAAAACGCTATATATTTTGCAGAAAAAGAAATTAATCTCTGTAACCTTAAAGATG	480		
QY	481	AAGTTTCTATCTCCAAAGTATGGCTACAGAAACCGTCCCAAAACATCTTACAGAGT	540		
Db	481	AAGTTTCTATCTCCAAAGTATGGCTACAGAAACCGTCCCAAAACATCTTACAGAGT	540		
QY	541	AAACCGGAAATCTTCCCTGAGGAAACAGTCTGAGTCCCAACCTCTTAACTTTGAA	600		
Db	541	AAACCGGAAATCTTCCCTGAGGAAACAGTCTGAGTCCCAACCTCTTAACTTTGAA	600		
QY	601	CTGTGAGAACTCTGAGGACAAAGACGCGATACAACTCTCAAAAGAGCTGTCTCATATG	660		
Db	601	CTGTGAGAACTCTGAGGACAAAGACGCGATACAACTCTCAAAAGAGCTGTCTCATATG	660		
QY	661	AATTGGATCTGATCTTCTGAAAGTACCGTATTAAGGCACTTATGCAAGTGGGAG	720		
Db	661	AATTGGATCTGATCTTCTGAAAGTACCGTATTAAGGCACTTATGCAAGTGGGAG	720		
QY	721	ATCAGAAATTTGTACAAATCACCCCTCAAGAAACAGGATGAAATCAATTTGATTTG	780		
Db	721	ATCAGAAATTTGTACAAATCACCCCTCAAGAAACAGGATGAAATCAATTTGATTTG	780		
QY	781	CAAAAAAGCGCTGTGTAATTTTCTGAGACGATGTAACTGAACTGAACTCATCAAC	840		
Db	781	CAAAAAAGCGCTGTGTAATTTTCTGAGACGATGTAACTGAACTGAACTCATCAAC	840		
QY	841	CCAGTAATATGATTTGAAACACCACTGAGAACGCTGACGCTAGAGGCAATCCAGAAAGT	900		
Db	841	CCAGTAATATGATTTGAAACACCACTGAGAACGCTGACGCTAGAGGCAATCCAGAAAGT	900		
QY	901	ATCAGGAGTGTCTGTTTCAAACTTGATGTGAGCACTGTGGCAAAATATCATGCA	960		
Db	901	ATCAGGAGTGTCTGTTTCAAACTTGATGTGAGCACTGTGGCAAAATATCATGCA	960		
QY	961	GCTTATTAACAG	1020		
Db	961	GCTTATTAACAG	1020		
QY	1021	AGGCTGAATCTGTATATATAAGCAAGAGCGCTTGGCAAGAGCCAACTAATACAGAT	1080		
Db	1021	AGGCTGAATCTGTATATATAAGCAAGAGCGCTTGGCAAGAGCCAACTAATACAGAT	1080		
QY	1081	GGGCTGGAAGTAAAGAAACATGATGATAGGCGAGCTCCAGACAGAAAAAGGTAG	1140		
Db	1081	GGGCTGGAAGTAAAGAAACATGATGATAGGCGAGCTCCAGACAGAAAAAGGTAG	1140		
QY	1141	ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGTGAATTAAGCAAACTGCTATGCT	1200		
Db	1141	ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGTGAATTAAGCAAACTGCTATGCT	1200		
QY	1201	CAGAGAACTCTGAGATATCTGAAAGTGTCTGATTAACCTAATTAAGCACTTACA	1260		
Db	1201	CAGAGAACTCTGAGATATCTGAAAGTGTCTGATTAACCTAATTAAGCACTTACA	1260		
QY	1261	AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTAAGTGTGCTGATGACACATGATG	1320		
Db	1261	AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTAAGTGTGCTGATGACACATGATG	1320		
QY	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATGGACGTTCTAAATGAGTAGATG	1380		
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATGGACGTTCTAAATGAGTAGATG	1380		
QY	1381	AATATTCGCTCTTCCAGAGAAATAGACTTACGCGAGATCCATGAGGCTTTAA	1440		
Db	1381	AATATTCGCTCTTCCAGAGAAATAGACTTACGCGAGATCCATGAGGCTTTAA	1440		
QY	1441	TATGTAAAGTGAAGAGATTCACCTCAATCAGTAGAGAGTAATTAAGCAAAATAT	1500		
Db	1441	TATGTAAAGTGAAGAGATTCACCTCAATCAGTAGAGAGTAATTAAGCAAAATAT	1500		
QY	1501	TTGGGAAAACCTATGGAAGAAAGGACGCTCCCACTTAAGCATGTAACTGAAATC	1560		
Db	1501	TTGGGAAAACCTATGGAAGAAAGGACGCTCCCACTTAAGCATGTAACTGAAATC	1560		
QY	1561	TATATATGAGCAATTTTCTGAGGACAGATTAATCAAGAGCGCTCCCTACAATA	1620		
Db	1561	TATATATGAGCAATTTTCTGAGGACAGATTAATCAAGAGCGCTCCCTACAATA	1620		
QY	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGAGATTTATCAAGAAAG	1680		
Db	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGAGATTTATCAAGAAAG	1680		
QY	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAACCAAGGAGC	1740		
Db	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAACCAAGGAGC	1740		
QY	1741	AGAATGTCAGTATGATATTTACTAATAGTGTGATGAGAAATTAACAAAGGTGAT	1800		
Db	1741	AGAATGTCAGTATGATATTTACTAATAGTGTGATGAGAAATTAACAAAGGTGAT	1800		
QY	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGATCTGTTCA	1860		
Db	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGATCTGTTCA	1860		
QY	1861	AAAGCAAACTGAACTTAAGCAAGCACTATAGCAATATGAACTCGAATTAATATCC	1920		
Db	1861	AAAGCAAACTGAACTTAAGCAAGCACTATAGCAATATGAACTCGAATTAATATCC	1920		
QY	1921	ACAATTTCAAAAGACCTTAAGAAAGTATGAGGCTGAGGAGAGAGTCTTACAGGCAATAT	1980		
Db	1921	ACAATTTCAAAAGACCTTAAGAAAGTATGAGGCTGAGGAGAGAGTCTTACAGGCAATAT	1980		
QY	1981	ATGCGCTTGAATAGTAGTCAATGAAATTAAGCCCACTTAATTTGATGATTTGCAAA	2040		
Db	1981	ATGCGCTTGAATAGTAGTCAATGAAATTAAGCCCACTTAATTTGATGATTTGCAAA	2040		
QY	2041	TTGATAGTGTCTTGAAGAGTGAAGATTAAGAAAAAAAGTCAACCAAAATGCCAGTCA	2100		
Db	2041	TTGATAGTGTCTTGAAGAGTGAAGATTAAGAAAAAAAGTCAACCAAAATGCCAGTCA	2100		
QY	2101	GGCAGAGAAAGCTCAACTCATGAGAGTAAAGAACTGCAACTGAGCCAAAGAA	2160		
Db	2101	GGCAGAGAAAGCTCAACTCATGAGAGTAAAGAACTGCAACTGAGCCAAAGAA	2160		



Db 2101 GGCACAGCAAAACCTACACTCATGGAAGTAAAGAACTGCACCTGGAGCCAGAGA 2160  
QY 2161 GTAACAAAGCAAAATGAACAGACAAAGTAAAAAGACATGACACGATCTTTCCAGAGCTGA 2220  
Db 2161 GTAACAAAGCAAAATGAACAGACAAAGTAAAAAGACATGACACGATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGCAACCTGGTCTTTTCTACTAGTGTTCAAATGATCCAGTGAACCTTAAAGAT 2280  
Db 2221 AGTTAAACAAATGCAACCTGGTCTTTTCTACTAGTGTTCAAATGATCCAGTGAACCTTAAAGAT 2280  
QY 2281 TTGTCAATCTAGCCTTCACAGAGAAAGAAAAGAGAAAGTGAACCTGAAACGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCTTCACAGAGAAAGAAAAGAGAAAGTGAACCTGAAACGTTAAAGTGT 2340  
QY 2341 CTATAATGCTGAAGAGCCCAAAAGATCTCATGTTAACTGAGAAAGGGTTTGCAAACTG 2400  
Db 2341 CTATAATGCTGAAGAGCCCAAAAGATCTCATGTTAACTGAGAAAGGGTTTGCAAACTG 2400  
QY 2401 AAAGATCTGAGAGAGATGAGACATTTTCATTTGCTGCTGATCTGATTTATGGCCTCAGG 2460  
Db 2401 AAAGATCTGAGAGAGATGAGATTTTCATTTGCTGCTGATCTGATTTATGGCCTCAGG 2460  
QY 2461 AAAGTATCTGCTTACTGTAAGTGTAGCCTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
Db 2461 AAAGTATCTGCTTACTGTAAGTGTAGCCTCTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
QY 2521 GTGTGAGTCAAGTGTGACGATTTTGAAAAACCCCAAGGAGCTAAATTCATGGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGACGATTTTGAAAAACCCCAAGGAGCTAAATTCATGGTTGTTCCAAAG 2580  
QY 2581 ATATATGAATGACACAGAGGCTTTAAAGTATGCAATTCATTTGGGACATGAGTTTACCACAGTC 2640  
Db 2581 ATATATGAATGACACAGAGGCTTTAAAGTATGCAATTCATTTGGGACATGAGTTTACCACAGTC 2640  
QY 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAACCTGATGCTAGTATTTGACAGATTCAT 2700  
Db 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAACCTGATGCTAGTATTTGACAGATTCAT 2700  
QY 2701 TCAAGGTTTCAAAAGCCGCACTCATTTGCTCTGTTTCAAAATCCAGAAATGACAGAAAGG 2760  
Db 2701 TCAAGGTTTCAAAAGCCGCACTCATTTGCTCTGTTTCAAAATCCAGAAATGACAGAAAGG 2760  
QY 2761 AATGTGCAATCTCTGCCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAATCTCTGCCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGATGAGTCTAATATCAGAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGATGAGTCTAATATCAGAGCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGACGAGCTTCTGTTGGTGTGTCAGAAAGATAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGACGAGCTTCTGTTGGTGTGTCAGAAAGATAGCCAGTTGATA 2940  
QY 2941 ATGCGAAATGTAGATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGATTTACAGAGCA 3000  
Db 2941 ATGCGAAATGTAGATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGATTTACAGAGCA 3000  
QY 3001 ACAGAAATCGACTATCTACTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060  
Db 3001 ACAGAAATCGACTATCTACTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060  
QY 3061 CACACACTTTTCCCATCACTCACTTTTGTAAACTTAATTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACACACTTTTCCCATCACTCACTTTTGTAAACTTAATTAAGAAAAATCTGCTAGAGG 3120  
QY 3121 AAAACCTTGAAGAACATTTCAATGTCACTGAAGAGAAATGAGAAATGAGAAACATTTCCAA 3180  
Db 3121 AAAACCTTGAAGAACATTTCAATGTCACTGAAGAGAAATGAGAAATGAGAAACATTTCCAA 3180  
QY 3181 GTACAGTGAACAAATAGCCGTAAATTAACATTTAGAGAAAAATGTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAACAAATAGCCGTAAATTAACATTTAGAGAAAAATGTTTAAAGAGCCAGCT 3240

QY 3241 CAAGCAATATTAATGAAGTATGCTTCCAGTACTATATGAAGTGGCTCCAGTATTAATGAAG 3300  
Db 3241 CAAGCAATATTAATGAAGTATGCTTCCAGTACTATATGAAGTGGCTCCAGTATTAATGAAG 3300  
QY 3301 TAGGTTCCAGTGAATGAAGAAACATCAAGCAGAACTAGTGTGAAGAAAGAGGCCCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGAATGAAGAAACATCAAGCAGAACTAGTGTGAAGAAAGAGGCCCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAAATTAAGGGGTTTTCACAACTGAGGCTCTTAACAAGAGTCTCTCGGAA 3420  
Db 3361 ATGCTATGCTTAAATTAAGGGGTTTTCACAACTGAGGCTCTTAACAAGAGTCTCTCGGAA 3420  
QY 3421 GTAATTTGAAGCATCTGAAATTAAGAAAGCAAGATATGAGAGTATGATTCAGACTGTTA 3480  
Db 3421 GTAATTTGAAGCATCTGAAATTAAGAAAGCAAGATATGAGAGTATGATTCAGACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTAAAGTAAAGAGGCTTAAGAGTATGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTAAAGTAAAGAGGCTTAAGAGTATGTC 3540  
QY 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGAATTAAGG 3600  
Db 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGAATTAAGG 3600  
QY 3601 AAGATCTAGTATTTGCTGAAATGACATTAAGGAAAGTCTGCTGTTTAAAGCAAAAGCG 3660  
Db 3601 AAGATCTAGTATTTGCTGAAATGACATTAAGGAAAGTCTGCTGTTTAAAGCAAAAGCG 3660  
QY 3661 TTCAGAAAGAGAGCTTAGAGAGTCTAGCCCTTTCACCCCTACACATNTGGCTCAGG 3720  
Db 3661 TTCAGAAAGAGAGCTTAGAGAGTCTAGCCCTTTCACCCCTACACATNTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGAGTCTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGAGTCTCTCAGAGAGAACTTATCTAGTGAAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTGTAAGTAAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTGTAAGTAAACAAATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCACTAGCACCGTGTGACAGAGTGTGCTAAGAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCACTAGCACCGTGTGACAGAGTGTGCTAAGAACACAGAGGAGAAATTTAT 3900  
QY 3901 TATCATTTGAAGATTAAGTAAATGATGACGATGAACAGGTAATATTTGGCAAGGCAATCTC 3960  
Db 3901 TATCATTTGAAGATTAAGTAAATGATGACGATGAACAGGTAATATTTGGCAAGGCAATCTC 3960  
QY 3961 AGGACATCACTTATGATGAGAAACAAATGTTCTGCTAGCTTGTCTTCTCAGAGTGCA 4020  
Db 3961 AGGACATCACTTATGATGAGAAACAAATGTTCTGCTAGCTTGTCTTCTCAGAGTGCA 4020  
QY 4021 GTGAATTTGAAGATGATGACGCAAAATCAAAACCCAGAGATCTTCTTCTGATTTGTTCTT 4080  
Db 4021 GTGAATTTGAAGATGATGACGCAAAATCAAAACCCAGAGATCTTCTTCTGATTTGTTCTT 4080  
QY 4081 CCAAAACAAATGAGGATCAAGTCTGAAGGCAAGGAGTGTGCTGAGATGACAAAGAAATTTGG 4140  
Db 4081 CCAAAACAAATGAGGATCAAGTCTGAAGGCAAGGAGTGTGCTGAGATGACAAAGAAATTTGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGAGAGGCTTGGAGAGAAATTAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGAGAGGCTTGGAGAGAAATTAATCAAGAGAGCAAGCA 4200  
QY 4201 TGGATTCAAACTTAAGGTGAAGAGCAGATCTGGGAGTGAAGTGAAGAAACGCTCTGAGG 4260  
Db 4201 TGGATTCAAACTTAAGGTGAAGAGCAGATCTGGGAGTGAAGTGAAGAAACGCTCTGAGG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTGACAGAGTGAATTTTAAACCACTCAGCAGAGAGATACCATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTGACAGAGTGAATTTTAAACCACTCAGCAGAGAGATACCATGC 4320

QY 4321 AACATACCTGATTAAGCTCCAGCAGGAAATGCGTGAATAGAACTGTGTAGAACACG 4380  
 |||||||  
 Db 4321 AACATACCTGATTAAGCTCCAGCAGGAAATGCGTGAATAGAACTGTGTAGAACACG 4380  
 QY 4381 ATGGAGCCGACCTTCTACAGCTACCTTCATCATAGGACTCTTCCCTTGAGG 4440  
 |||||||  
 Db 4381 ATGGAGCCGACCTTCTACAGCTACCTTCATCATAGGACTCTTCCCTTGAGG 4440  
 QY 4441 ACCGCGAAATCCAGAACAGCATCAGAAAAAGCAGTAACTTCAACAGAAAAATA 4500  
 |||||||  
 Db 4441 ACCGCGAAATCCAGAACAGCATCAGAAAAAGCAGTAACTTCAACAGAAAAATA 4500  
 QY 4501 GTGAATACCTTATAGCCAAATCCAGAAAGCCTTCTGCTGANAAGTTGAGGTGCTG 4560  
 |||||||  
 Db 4501 GTGAATACCTTATAGCCAAATCCAGAAAGCCTTCTGCTGANAAGTTGAGGTGCTG 4560  
 QY 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTAAAT 4620  
 |||||||  
 Db 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTAAAT 4620  
 QY 4621 GCCCATCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
 |||||||  
 Db 4621 GCCCATCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
 QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGACACAGCTGGAAG 4740  
 |||||||  
 Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGACACAGCTGGAAG 4740  
 QY 4741 AGCTGTGGCCACAGATTTGACGGAACATCTTACTGCCAAGCAGATCTAGAGGAA 4800  
 |||||||  
 Db 4741 AGCTGTGGCCACAGATTTGACGGAACATCTTACTGCCAAGCAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGCAATCTGCAATCAGCTCTCTGATGACCTGCAATCTGATCTCTG 4860  
 |||||||  
 Db 4801 CCCCTTACCTGCAATCTGCAATCAGCTCTCTGATGACCTGCAATCTGATCTCTG 4860  
 QY 4861 AAGACAGAGCCAGAGTACGCTGTGTGGCAACATCATCTTCAACCTCTGCAATGTA 4920  
 |||||||  
 Db 4861 AAGACAGAGCCAGAGTACGCTGTGTGGCAACATCATCTTCAACCTCTGCAATGTA 4920  
 QY 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGATCCAGCTGCTCATACTACTG 4980  
 |||||||  
 Db 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGATCCAGCTGCTCATACTACTG 4980  
 QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAACCAATTTGACAG 5040  
 |||||||  
 Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAACCAATTTGACAG 5040  
 QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGGGTGCTGCGCTGACCCCAAGAG 5100  
 |||||||  
 Db 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGGGTGCTGCGCTGACCCCAAGAG 5100  
 QY 5101 AATTTATGCTGTGATCAAGTTTGCAGAAACACACATCACTTAACTAATTAATTA 5160  
 |||||||  
 Db 5101 AATTTATGCTGTGATCAAGTTTGCAGAAACACACATCACTTAACTAATTAATTA 5160  
 QY 5161 CTGAAGAGACTCTCTATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGACAC 5220  
 |||||||  
 Db 5161 CTGAAGAGACTCTCTATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGACAC 5220  
 QY 5221 TGAATATTTTGTAGAAATTTGGGAGGAAATGGGTAGTTACTTATTTCTGGGTGACCC 5280  
 |||||||  
 Db 5221 TGAATATTTTGTAGAAATTTGGGAGGAAATGGGTAGTTACTTATTTCTGGGTGACCC 5280  
 QY 5281 AGTCTATTAAAGAAAGAAATCTGTAATGAGCATGATTTTGAAGTCAGAGGAGATGTG 5340  
 |||||||  
 Db 5281 AGTCTATTAAAGAAAGAAATCTGTAATGAGCATGATTTTGAAGTCAGAGGAGATGTG 5340  
 QY 5341 TCAATGGAAGAAACCAAGGTCACAAAGGTCAGAGCAAGAGATCCAGAGAGAAAGATCT 5400  
 |||||||  
 Db 5341 TCAATGGAAGAAACCAAGGTCACAAAGGTCAGAGCAAGAGATCCAGAGAGAAAGATCT 5400  
 QY 5401 TCAGGGGGCTAGAAATCTTGTGTATGGGCCCTTCAACAATGCCACAGATCAACTG 5460

Db 5401 TCAGGGGGCTAGAAATCTTGTGTATGGGCCCTTCAACAATGCCACAGATCAACTG 5460  
 |||||||  
 QY 5461 AATGATGATGACAGCTGTGTGTGCTTCTGTGTGTAAGAGGCTTTCATCATCACCTTG 5520  
 |||||||  
 Db 5461 AATGATGATGACAGCTGTGTGTGCTTCTGTGTGTAAGAGGCTTTCATCATCACCTTG 5520  
 QY 5521 GCACAGGTGTCACACCAATTTGTTGTGAGCAGCATGCTGTGACAGAGAGCAATGCTG 5580  
 |||||||  
 Db 5521 GCACAGGTGTCACACCAATTTGTTGTGAGCAGCATGCTGTGACAGAGAGCAATGCTG 5580  
 QY 5581 TCCATGCAATTTGGGAGAGTGTGAGCAGCTGTGTGACCCGAGAGTGGTGGACA 5640  
 |||||||  
 Db 5581 TCCATGCAATTTGGGAGAGTGTGAGCAGCTGTGTGACCCGAGAGTGGTGGACA 5640  
 QY 5641 GTGTAGCCTCTACAGTGCAGAGCTGTGAGCAGCTGTGATACCTGATACCCAGACCA 5700  
 |||||||  
 Db 5641 GTGTAGCCTCTACAGTGCAGAGCTGTGAGCAGCTGTGATACCTGATACCCAGACCA 5700  
 QY 5701 GCCACTACTGA 5711  
 |||||||  
 Db 5701 GCCACTACTGA 5711

## RESULT 14

ID T18311 standard; cDNA; 5914 BP.  
 AC T18311;  
 DT 05-JUN-1996 (first entry)  
 DE BRCA1 gene nonsense allele.  
 KW BRCA1; breast cancer; ovary cancer; predisposing gene;  
 OS Homo sapiens.  
 FH key Location/Qualifiers  
 FT cds 120..4058  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /\*tag= /note= "wild-type BRCA1 has C at position 4056"  
 PN W09605307-A2.  
 PD 22-FEB-1996.  
 PF 11-AUG-1995: U10203.  
 PR 12-AUG-1994: US-289221.  
 PR 02-SEP-1994: US-300266.  
 PR 16-SEP-1994: US-308104.  
 PR 29-NOV-1994: US-348824.  
 PR 24-MAR-1995: US-409305.  
 PR 07-JUN-1995: US-488011.  
 PR 07-JUN-1995: US-483554.  
 PR 07-JUN-1995: US-487002.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PI Futrel AP, Goldgar DE, Harsman KD, Kamb A, Miki Y,  
 PI Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV,  
 PI Wiseman RW.  
 DR WPI; 96-139703/14.  
 PT New isolated human cancer predisposing gene, BRCA1 - used to develop  
 PT prods. for diagnosis, prognosis and therapy of cancers, partic.  
 PT breast and ovarian cancers  
 PS Claim 9, Page 108-117; 190pp; English.  
 CC A BRCA1 susceptibility allele (T18311) was detected in a kindred  
 CC having a nearly equal incidence of breast and ovarian cancer.  
 CC A C to T substitution in exon 11 (position 4056 of the wild-type  
 CC BRCA1, see T18310) converted a Gln codon to a stop codon,  
 CC resulting in a BRCA1 polypeptide lacking 551 C-terminal residues.  
 CC cosegregation of the allele with disease and its absence in  
 CC controls were observed. Probes based on this and other  
 CC susceptibility alleles (see also T18312-14) can be used to  
 CC diagnose predisposition to cancer, partic. breast and ovarian  
 SQ Sequence 5914 BP; 2006 A; 1155 C; 1316 G; 1437 T;

Query Match 99.9%; Score 5707.8; DB 1; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACCTCCGCGACCCCGCACAGCGCTGCGGGGTTCTCGATTAACCTGGCC 60  
DB 1 AGCTGCTGAGACCTCCGCGACCCCGCACAGCGCTGCGGGGTTCTCGATTAACCTGGCC 60  
QY 61 CCGGCTGAGAGGCGCTTCAACCTCTGCTGCGTAAAGTTTCATTTGAGACAGAAAGAAA 120  
DB 61 CCGGCTGAGAGGCGCTTCAACCTCTGCTGCGTAAAGTTTCATTTGAGACAGAAAGAAA 120  
QY 121 TGGATTTATCTGCTCTTCCGCTGGAAGAATGCAATTAATGCTATTAATGCGAGAAA 180  
DB 121 TGGATTTATCTGCTCTTCCGCTGGAAGAATGCAATTAATGCTATTAATGCGAGAAA 180  
QY 181 TCTTAGAGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCCAAGTGTGACC 240  
DB 181 TCTTAGAGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCCAAGTGTGACC 240  
QY 241 ACATTTTTCGAAAATTTTGCATGCTGAACCTTCTCAACAGAGAAAGGCGCTTCAAGT 300  
DB 241 ACATTTTTCGAAAATTTTGCATGCTGAACCTTCTCAACAGAGAAAGGCGCTTCAAGT 300  
QY 301 GTCCCTTATGTAAGATGATATACCAAGAGCGCTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCCCTTATGTAAGATGATATACCAAGAGCGCTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACCTGTGAGAGGTATGTAAGATTTGCTTTCACCTTTCAGCAGAGTTTGGAGT 420  
DB 361 AACCTGTGAGAGGTATGTAAGATTTGCTTTCACCTTTCAGCAGAGTTTGGAGT 420  
QY 421 ATGCAAAACAGCTATATTTTGCAAAAGAAATTAATCTCTGTAACATCTAAAGATG 480  
DB 421 ATGCAAAACAGCTATATTTTGCAAAAGAAATTAATCTCTGTAACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGATCTTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGATCTTACAGAGTG 540  
QY 541 AACCGAAAATCTCTCTGAGGAAACCAAGTCAAGTCCAACTCTTAACCTTGGAA 600  
DB 541 AACCGAAAATCTCTCTGAGGAAACCAAGTCTCAAGTCTCAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGAAAGCAGCGGATACAACTCAAAAGCGTCTGTACATG 660  
DB 601 CTGTGAGAACTCTGAGGAAAGCAGCGGATACAACTCAAAAGCGTCTGTACATG 660  
QY 661 AATTGGATCTGATTTCTTGAAGATCCGTTAATAGGCAACTTATGCAAGTGGGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATCCGTTAATAGGCAACTTATGCAAGTGGGAG 720  
QY 721 ATCAGAAATGTTTCAAAATCAACCCCTCAAGGACAGGAGTAAATCACTGTTGATCTG 780  
DB 721 ATCAGAAATGTTTCAAAATCAACCCCTCAAGGACAGGAGTAAATCACTGTTGATCTG 780  
QY 781 CAAAAAAGCGCTGTTGAAATTTTCTGAGAGGATGTAACAATTAATCAATCATCAAC 840  
DB 781 CAAAAAAGCGCTGTTGAAATTTTCTGAGAGGATGTAACAATTAATCAATCATCAAC 840  
QY 841 CCAGTAAATTAATGATTTGAACACCACTGAGAAAGCGTCAAGTGGAGGATCCAGAAAAGT 900  
DB 841 CCAGTAAATTAATGATTTGAACACCACTGAGAAAGCGTCAAGTGGAGGATCCAGAAAAGT 900  
QY 901 ATCAGAGGATGTTGTTCAAACTGATGAGGATGAGGCAATGAGCAATTAATGATGCA 960  
DB 901 ATCAGAGGATGTTGTTCAAACTGATGAGGATGAGGCAATGAGCAATTAATGATGCA 960  
QY 961 GCTCATTAACAGCATGAGAACAGAGTTTATTAATCACTAAAGACAGATGATGAGAAA 1020  
DB 961 GCTCATTAACAGCATGAGAACAGAGTTTATTAATCACTAAAGACAGATGATGAGAAA 1020

QY 1021 AGCGTGAATTTCTGTAATTAAGCAACAGCTGCTTACGAGAGGACCAATTAACGAT 1080  
DB 1021 AGCGTGAATTTCTGTAATTAAGCAACAGCTGCTTACGAGAGGACCAATTAACGAT 1080  
QY 1081 GGGCTGGAATGAGAAACATGTAATGATAGGCGACTCCAGCAGAGAAAAGGATG 1140  
DB 1081 GGGCTGGAATGAGAAACATGTAATGATAGGCGACTCCAGCAGAGAAAAGGATG 1140  
QY 1141 ATCTGAATGCTGATCCCGTGTGTGAGAGAAAAGATGGAATTAACAGAAATGCTGCT 1200  
DB 1141 ATCTGAATGCTGATCCCGTGTGTGAGAGAAAAGATGGAATTAACAGAAATGCTGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACCTTAATAGCAGATTGCA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACCTTAATAGCAGATTGCA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAGTGTGATGAACGTTGAGTTCGATGACATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAGTGTGATGAACGTTGAGTTCGATGACATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTAAGAGTTCTTAATGAGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTAAGAGTTCTTAATGAGTAGATG 1380  
QY 1381 AATATTCTGCTTCTCAGAGAAATTAAGATTACTGCGCAGTGTCTCATGAGGCTTTAA 1440  
DB 1381 AATATTCTGCTTCTCAGAGAAATTAAGATTACTGCGCAGTGTCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAGAGGAAAGGTTTCACTCCAAATCAGTAGAGATTAATTAAGAGCAAAATAT 1500  
DB 1441 TATGTAAGAGGAAAGGTTTCACTCCAAATCAGTAGAGATTAATTAAGAGCAAAATAT 1500  
QY 1501 TTGGGAAAACCTATCGGAGAGAGGCAAGCGTCCCAACTTAAGCATGTAAGTAAATC 1560  
DB 1501 TTGGGAAAACCTATCGGAGAGAGGCAAGCGTCCCAACTTAAGCATGTAAGTAAATC 1560  
QY 1561 TAATTTAGAGACATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
DB 1561 TAATTTAGAGACATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
QY 1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCGTTCATCCGAGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCGTTCATCCGAGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACCTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGACCTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATTTTACTAATAGTGTGCTCATGAGATTAACCAAGGAGC 1800  
DB 1741 AGAATGCTCAAGTGAATTTTACTAATAGTGTGCTCATGAGATTAACCAAGGAGC 1800  
QY 1801 CTATTCGAATGAGAAATTAATCTTAACCAATAGAAATACGAGAAAGAAATCTCTTCA 1860  
DB 1801 CTATTCGAATGAGAAATTAATCTTAACCAATAGAAATACGAGAAAGAAATCTCTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTATTAAGCAGAGTATTAACCAATATGAACTGAAATTAATATCC 1920  
DB 1861 AAACGAAAGCTGAACCTATTAAGCAGAGTATTAACCAATATGAACTGAAATTAATATCC 1920  
QY 1921 ACAATTTAAAAGCAGCTTAATAAGATAGGCTGAGAGGAAAGTCTTCAACAGCATATTC 1980  
DB 1921 ACAATTTAAAAGCAGCTTAATAAGATAGGCTGAGAGGAAAGTCTTCAACAGCATATTC 1980  
QY 1981 ATGCGCTTGAACCTGATGATGTAAGAAATCTAAGCCACAGCTAATTTGACGAATGGA 2040  
DB 1981 ATGCGCTTGAACCTGATGATGTAAGAAATCTAAGCCACAGCTAATTTGACGAATGGA 2040  
QY 2041 TTGATAGTTGTTTACAGAGTGAAGAGATTAAGAAAAAGTACAAACCAATGACAGTCA 2100  
DB 2041 TTGATAGTTGTTTACAGAGTGAAGAGATTAAGAAAAAGTACAAACCAATGACAGTCA 2100  
QY 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGCACTGAGCCAGAGAA 2160

```
Db 2101 GGGACGACAAACCTCACTGAGAGGTAAAGAACTGCGACATGAGCCCAAGAGA 2160
QY 2161 GTACACAGCCAAATGACAGACAACTAAAAGACATGACAGGACTACTTCCAGAGCTGA 2220
Db 2161 GTACACAGCCAAATGACAGACAACTAAAAGACATGACAGGACTACTTCCAGAGCTGA 2220
QY 2221 AGTTAACAAATGCACTGGTTCCTTTACTAAGTGTCAAAATACCAAGTAAAGAT 2280
Db 2221 AGTTAACAAATGCACTGGTTCCTTTACTAAGTGTCAAAATACCAAGTAAAGAT 2280
QY 2281 TTGTCAATCCTAGCCTTCCAGAGAGAAAAGAAAGAACTGAACCTAAAGGT 2340
Db 2281 TTGTCAATCCTAGCCTTCCAGAGAGAAAAGAAAGAACTGAACCTAAAGGT 2340
QY 2341 CTATATATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400
Db 2341 CTATATATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400
QY 2401 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTTATGCACTCAGG 2460
Db 2401 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTTATGCACTCAGG 2460
QY 2461 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTTATGCACTCAGG 2520
Db 2461 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTTATGCACTCAGG 2520
QY 2521 GTGTGAGTCAGTGTGCAGCATTTTGAAGAAACCCCAAGGACTAATTCATGTTTCCAAAG 2580
Db 2521 GTGTGAGTCAGTGTGCAGCATTTTGAAGAAACCCCAAGGACTAATTCATGTTTCCAAAG 2580
QY 2581 ATATATGAATGACACAGAGGCTTATAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
Db 2581 ATATATGAATGACACAGAGGCTTATAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
QY 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTGATGCTACATATTTGAGAAATCAT 2700
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTGATGCTACATATTTGAGAAATCAT 2700
QY 2701 TCAGAGTTTCAAAAGCCGCACTATTTGCTGTGTTTCAAAATCCAGAAATGCAAGAGG 2760
Db 2701 TCAGAGTTTCAAAAGCCGCACTATTTGCTGTGTTTCAAAATCCAGAAATGCAAGAGG 2760
QY 2761 AATGTCAACATTTCTGCCCACCTGCGGCTCTTAAGAAACAAGTCCAAAGTCACTT 2820
Db 2761 AATGTCAACATTTCTGCCCACCTGCGGCTCTTAAGAAACAAGTCCAAAGTCACTT 2820
QY 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGATGAGTCTAATATCAGGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGATGAGTCTAATATCAGGCTGTAC 2880
QY 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940
Db 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940
QY 2941 ATGCCAAATGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAGAGCA 3000
Db 2941 ATGCCAAATGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAGAGCA 3000
QY 3001 ACGAAACTGAGACTCATTTACCAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060
Db 3001 ACGAAACTGAGACTCATTTACCAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAAGAAAACTCGTAGAGG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAAGAAAACTCGTAGAGG 3120
QY 3121 AAAACTTTGAGAAACTTCAATGTCACTGACCTGAAGAGAAAGGAAATGAGAAATTCCTCA 3180
Db 3121 AAAACTTTGAGAAACTTCAATGTCACTGACCTGAAGAGAAAGGAAATGAGAAATTCCTCA 3180
QY 3181 GTACAGTGAACAATTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTGAACAATTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTGAACAATTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGCT 3240
QY 3241 CAAGCAATATTAATGAAAGTAGTTCCAGTACTAATGAAGTGGGCTCCAGATTAATGAAA 3300
Db 3241 CAAGCAATATTAATGAAAGTAGTTCCAGTACTAATGAAGTGGGCTCCAGATTAATGAAA 3300
QY 3301 TAGGTTCCAGTGAATGAACATTCAGAGAGACTAGGTGAAGAAAGAGGCCCCAAATGTA 3360
Db 3301 TAGGTTCCAGTGAATGAACATTCAGAGAGACTAGGTGAAGAAAGAGGCCCCAAATGTA 3360
QY 3361 ATGCTATGCTTAGATTAAGGGGTTTGGAACTGAGGCTCTAATAACAAAGTCTCCGGA 3420
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTGGAACTGAGGCTCTAATAACAAAGTCTCCGGA 3420
QY 3421 GTAATTTGAAGCATCTGAAATTAAGAAACAGAAATATGAAGAGTAGTTCAGACTGTGA 3480
Db 3421 GTAATTTGAAGCATCTGAAATTAAGAAACAGAAATATGAAGAGTAGTTCAGACTGTGA 3480
QY 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTAACAGCCTATGGGAATAGTC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTAACAGCCTATGGGAATAGTC 3540
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGAGTGAATTAAG 3600
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGAGTGAATTAAG 3600
QY 3601 AAGATCTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTACCAAAAGCG 3660
Db 3601 AAGATCTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTACCAAAAGCG 3660
QY 3661 TCCAGAAAGAGAGCTTAGAGAGAGCTAGACCTTACCCCTTACACATACACTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCTTAGAGAGAGCTAGACCTTACCCCTTACACATACACTTGGCTCAGG 3720
QY 3721 GTTACCGAAGAGGAGGCGCAAGAAATTAAGTCTCAGAAAGAGAACTTATCTAGAGATG 3780
Db 3721 GTTACCGAAGAGGAGGCGCAAGAAATTAAGTCTCAGAAAGAGAACTTATCTAGAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTGAAGTAAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTGAAGTAAACAATATACCTTCTCAGT 3840
QY 3841 CTACTAGGATTAACAGAGCTTGTCTACGAGTGTCTGCTAAGAAACAAGAGAAATTAAT 3900
Db 3841 CTACTAGGATTAACAGAGCTTGTCTACGAGTGTCTGCTAAGAAACAAGAGAAATTAAT 3900
QY 3901 TATCATTTGAAGATTAACCTTAATTAAGTCACTGAGTACCAAGATTAATTTGGCAAGCATCTC 3960
Db 3901 TATCATTTGAAGATTAACCTTAATTAAGTCACTGAGTACCAAGATTAATTTGGCAAGCATCTC 3960
QY 3961 AGGACATCACTTATGAGAGAAACAAATGTTGCTGCTAGCTTGTCTTCCAGAGTCA 4020
Db 3961 AGGACATCACTTATGAGAGAAACAAATGTTGCTGCTAGCTTGTCTTCCAGAGTCA 4020
QY 4021 GTGAATTTGAAGACTGACTGCAATTAACAACACAGAGATCTTCTGATGTTGTTCTT 4080
Db 4021 GTGAATTTGAAGACTGACTGCAATTAACAACACAGAGATCTTCTGATGTTGTTCTT 4080
QY 4081 CCAACAATTAAGAGCATCTGACTGAAAGCCAGAGAGTTGTTGATGATGATGATGATG 4140
Db 4081 CCAACAATTAAGAGCATCTGACTGAAAGCCAGAGAGTTGTTGATGATGATGATGATG 4140
QY 4141 TTTCAATGATGAAGAAAGAGAGAGGCTTGGAAAGAAATATATCAAGAGAGCA 4200
Db 4141 TTTCAATGATGAAGAAAGAGAGAGGCTTGGAAAGAAATATATCAAGAGAGCA 4200
QY 4201 TGGATTTCAACTTAGTGAAGAGCATCTGGGCTGGAAGAGTGAAGTGAAGTGAAG 4260
Db 4201 TGGATTTCAACTTAGTGAAGAGCATCTGGGCTGGAAGAGTGAAGTGAAGTGAAG 4260
QY 4261 ACTGCTCAGAGGCTATCTCTGAGAGTGAATTAACCACTCAGAGAGGATACATG 4320
Db 4261 ACTGCTCAGAGGCTATCTCTGAGAGTGAATTAACCACTCAGAGAGGATACATG 4320
```

QY 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGATAGAAAGCTGTGTGAACAGC 4380  
 DB 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGATAGAAAGCTGTGTGAACAGC 4380  
 QY 4381 ATGGAGACCGCTTCTTAACAGGACCTTCATCATAGTGAAGCTGTGAGCCTTGAGG 4440  
 DB 4381 ATGGAGACCGCTTCTTAACAGGACCTTCATCATAGTGAAGCTGTGAGCCTTGAGG 4440  
 QY 4441 ACCTGGGAAATCCAGAACAGACATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA 4500  
 DB 4441 ACCTGGGAAATCCAGAACAGACATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA 4500  
 QY 4501 GTGAATACCTATTAAGCAGAAATCCAGAGCCTTTCTGCTGACAGTTGAGTGTCTG 4560  
 DB 4501 GTGAATACCTATTAAGCAGAAATCCAGAGCCTTTCTGCTGACAGTTGAGTGTCTG 4560  
 QY 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTTTCTAAAT 4620  
 DB 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTTTCTAAAT 4620  
 QY 4621 GCCCATCATTAAGTATGATAGTGTGTACATGACAGATTGCTGTGGAGTCTTCAGAAATGAA 4680  
 DB 4621 GCCCATCATTAAGTATGATAGTGTGTACATGACAGATTGCTGTGGAGTCTTCAGAAATGAA 4680  
 QY 4681 ACTACCATCATCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGACAAAGCTGGAAG 4740  
 DB 4681 ACTACCATCATCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGACAAAGCTGGAAG 4740  
 QY 4741 AGTCTGGGACACAGATTTAGCGAAACATCTTACTGCCAAGCAGATCTGAGAGGAA 4800  
 DB 4741 AGTCTGGGACACAGATTTAGCGAAACATCTTACTGCCAAGCAGATCTGAGAGGAA 4800  
 QY 4801 CCCCTTACCTGGAATCTGGAATGAGCTCTCTCTGATGACCTGGAATCTGATCTCTG 4860  
 DB 4801 CCCCTTACCTGGAATCTGGAATGAGCTCTCTCTGATGACCTGGAATCTGATCTCTG 4860  
 QY 4861 AAGACAGAGCCCGCAGAGTCTGCTGTGCGCAACATACATCTTCAACCTCTGCAATGA 4920  
 DB 4861 AAGACAGAGCCCGCAGAGTCTGCTGTGCGCAACATACATCTTCAACCTCTGCAATGA 4920  
 QY 4921 AAGTCCCAATGAAGTGAAGTGAAGTCCCAAGTCCAGTGGCTGCTCATACTG 4980  
 DB 4921 AAGTCCCAATGAAGTGAAGTGAAGTCCCAAGTCCAGTGGCTGCTCATACTG 4980  
 QY 4981 ATACTGCTGGGTAAATGAATGAAGAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 5040  
 DB 4981 ATACTGCTGGGTAAATGAATGAAGAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 5040  
 QY 5041 CTTCACAG 5100  
 DB 5041 CTTCACAG 5100  
 QY 5101 AATTATGCTGCTGATCAATTTGCGAGAAACACCAATCACTTAACTTAATTA 5160  
 DB 5101 AATTATGCTGCTGATCAATTTGCGAGAAACACCAATCACTTAACTTAATTA 5160  
 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAGAAAGAGTGTGATGTTGTTGTTGTTGTTGTTG 5220  
 DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAGAAAGAGTGTGATGTTGTTGTTGTTGTTGTTG 5220  
 QY 5221 TGAATAATTTTCTAGAGAAATGCGGAGAGAAATGAGTGTGTTGTTGTTGTTGTTGTTG 5280  
 DB 5221 TGAATAATTTTCTAGAGAAATGCGGAGAGAAATGAGTGTGTTGTTGTTGTTGTTGTTG 5280  
 QY 5281 AGCTATTAAGAAAGAAAGAAAGTGTGAATGAGATGTTTGAAGTGTGAGAGAGATGTGG 5340  
 DB 5281 AGCTATTAAGAAAGAAAGAAAGTGTGAATGAGATGTTTGAAGTGTGAGAGAGATGTGG 5340  
 QY 5341 TCATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGATCT 5400  
 DB 5341 TCATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGATCT 5400

QY 5401 TCAGGGGGCTAGAAATCTGTGCTATGAGGCTTCACCAACATGCCACAGATCAACTGG 5460  
 DB 5401 TCAGGGGGCTAGAAATCTGTGCTATGAGGCTTCACCAACATGCCACAGATCAACTGG 5460  
 QY 5461 AATGATGTGACAGCTGTGTGTGTGCTTCTGTGTGAGAGAGCTTTCATCATCACTG 5520  
 DB 5461 AATGATGTGACAGCTGTGTGTGTGCTTCTGTGTGAGAGAGCTTTCATCATCACTG 5520  
 QY 5521 GCACAGGTGTCCACCAATTTGTTGTGACAGCAGATGCTTGACAGAGACAAATGCT 5580  
 DB 5521 GCACAGGTGTCCACCAATTTGTTGTGACAGCAGATGCTTGACAGAGACAAATGCT 5580  
 QY 5581 TCCATGCAATTTGGGAGATGTGTGAGCAGCCTGTTGTTGTTGTTGTTGTTGTTGTTG 5640  
 DB 5581 TCCATGCAATTTGGGAGATGTGTGAGCAGCCTGTTGTTGTTGTTGTTGTTGTTGTTG 5640  
 QY 5641 GTGTAGACCTCTACAGAGTCCAGAGAGCTGAGACCTGATGATACCCCAATGCTG 5700  
 DB 5641 GTGTAGACCTCTACAGAGTCCAGAGAGCTGAGACCTGATGATACCCCAATGCTG 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711  
 RESULT 15  
 ID T1813 standard; cDNA; 5914 BP.  
 AC T1813;  
 DT 05-JUN-1996 (first entry)  
 DE BRCA1 gene missense allele.  
 KW BRCA1; breast cancer; ovary cancer; predisposing gene;  
 OS Homo sapiens.  
 FH Location/Qualifiers  
 FT key 120..5711  
 FT cds  
 FT allele 5443  
 FT /tag- b  
 FT /note- "t at position 5443 of wild-type  
 PN BRCA1 is substituted by g"  
 PD MO9605307-A2.  
 PD 22-FEB-1996.  
 PE 11-AUG-1995; 010203.  
 PR 12-AUG-1994; US-289221.  
 PR 02-SEP-1994; US-300266.  
 PR 16-SEP-1994; US-308104.  
 PR 29-NOV-1994; US-348824.  
 PR 24-MAR-1995; US-409305.  
 PR 07-JUN-1995; US-488011.  
 PR 07-JUN-1995; US-483554.  
 PR 07-JUN-1995; US-487002.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (UTAH-) UNIV UTAH RES FOUND.  
 PA (USSR-) US DEPT HEALTH & HUMAN SERVICES.  
 PA Futrelle AP, Goldgar DE, Hartsman KD, Kamb A, Miki Y;  
 PI Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;  
 PI Wiseman RW;  
 DR MPI: 96-139703/14.  
 PT New isolated human cancer predisposing gene, BRCA1 - used to develop  
 PT prods. for diagnosis, prognosis and therapy of cancers, partic.  
 PT breast and ovarian cancers  
 PS Claim 9; Page 108-117; 190pp; English.  
 CC A BRCA1 susceptibility allele (T1813) was detected in a kindred  
 CC that displayed early age of breast cancer onset. A T to G  
 CC mutation in exon 21 (position 5443 in the wild-type BRCA1  
 CC gene, see T1810) is potentially disruptive as it causes the  
 CC replacement of small, hydrophobic Met by large, charged Arg.  
 CC cosegregation of the allele with disease and its absence in  
 CC controls were observed. Probes based on this and other  
 CC susceptibility alleles (see also T1811-12 and T1814) can be  
 CC used to diagnose predisposition to cancer, partic. breast and  
 CC ovarian cancer..

Seq	Sequence	5914 BP;	2006 A;	1156 C;	1317 G;	1435 T;
Query Match 99.9%; Score 5707.8; DB 1; Length 5914;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
OY	1	ACCTGCTAGACTTCTTGAGACCCCGACAGGCTGTGGGTTTCTAGATTAACGTGGCC	60			
Db	1	ACCTGCTAGACTTCTTGAGACCCCGACAGGCTGTGGGTTTCTAGATTAACGTGGCC	60			
OY	61	CTGCGCTAGAGAGGCTTACCCCTGCTCTGGGTTTCAATTCATTGGAACAGAAAGAA	120			
Db	61	CTGCGCTAGAGAGGCTTACCCCTGCTCTGGGTTTCAATTCATTGGAACAGAAAGAA	120			
OY	121	TGAGATTATCTGCTCTTCCGCTTGAAGAAAGTACAAAATGCTAATTAATGCTATGAGAAA	180			
Db	121	TGAGATTATCTGCTCTTCCGCTTGAAGAAAGTACAAAATGCTAATTAATGCTATGAGAAA	180			
OY	181	TCTTAGAGTCTCCATCTGCTCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC	240			
Db	181	TCTTAGAGTCTCCATCTGCTCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC	240			
OY	241	ACATATTTTGCAGATTTTGGATGCTGAACTTCTCAACAGAAAGAGGCTTCCAGT	300			
Db	241	ACATATTTTGCAGATTTTGGATGCTGAACTTCTCAACAGAAAGAGGCTTCCAGT	300			
OY	301	GTCCTTATGTAGAAATGATATACCAAGAGGCTTACAAAGATACAGATTTATGTC	360			
Db	301	GTCCTTATGTAGAAATGATATACCAAGAGGCTTACAAAGATACAGATTTATGTC	360			
OY	361	AACCTTTGAAGAGCTATTTGAAATCATTTGTCTTTTCAAGCTTGACACAGGTTGGAGT	420			
Db	361	AACCTTTGAAGAGCTATTTGAAATCATTTGTCTTTTCAAGCTTGACACAGGTTGGAGT	420			
OY	421	ATGCAAGAGCTATATTTTTCGAAAAGAAATATACCTCTCTGAAACATCTAAAGATG	480			
Db	421	ATGCAAGAGCTATATTTTTCGAAAAGAAATATACCTCTCTGAAACATCTAAAGATG	480			
OY	481	AACTTTCTATCATCCAAAGTATGCGCTACAGAAACCGTCCAAAGACTTCTACAGAGT	540			
Db	481	AACTTTCTATCATCCAAAGTATGCGCTACAGAAACCGTCCAAAGACTTCTACAGAGT	540			
OY	541	AACCGGAAATCTCTCCGAGGAAACAGTCTCACTGTCGCAACCTCTAACTTGGAA	600			
Db	541	AACCGGAAATCTCTCTCCGAGGAAACAGTCTCACTGTCGCAACCTCTAACTTGGAA	600			
OY	601	CTGTAGAGACTCTGAGGACAAAGCAGGATACAACTCTCAAAAGAGCTGTCTACATTG	660			
Db	601	CTGTAGAGACTCTGAGGACAAAGCAGGATACAACTCTCAAAAGAGCTGTCTACATTG	660			
OY	661	AATGGAGTCTGATCTTCTGAAGATACCGTTAATAGGCACTTATGCAAGTGGGAG	720			
Db	661	AATGGAGTCTGATCTTCTGAAGATACCGTTAATAGGCACTTATGCAAGTGGGAG	720			
OY	721	ATCAGAAATTTTAAACACCCCTCAAGGAAACCGAGATGAATACAGTTTGGATTCTG	780			
Db	721	ATCAGAAATTTTAAACACCCCTCAAGGAAACCGAGATGAATACAGTTTGGATTCTG	780			
OY	781	CAAAAAGGCTCTGTGAAATTTTCTGAGACGATATACAAATCTGAAACATCATCAAC	840			
Db	781	CAAAAAGGCTCTGTGAAATTTTCTGAGACGATATACAAATCTGAAACATCATCAAC	840			
OY	841	CCAGTAATTAATGATTGAACACCACTGAGAGCGTCACTGAGAGCATCCAGAAAGT	900			
Db	841	CCAGTAATTAATGATTGAACACCACTGAGAGCGTCACTGAGAGCATCCAGAAAGT	900			
OY	901	ATCAGAGTCTGTTTCAAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	960			
Db	901	ATCAGAGTCTGTTTCAAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	960			
OY	961	GCTCATTCAGCATGAGAAACAGATTTATTAATCACTAAAGCAGAAATGATGTAGAA	1020			
Db	961	GCTCATTCAGCATGAGAAACAGATTTATTAATCACTAAAGCAGAAATGATGTAGAA	1020			
OY	1021	AGGCTGAATTTCTGTAAATTAAGCAACAGCTGGCTTACCAAGAGGAGGAGGAGGAGG	1080			
Db	1021	AGGCTGAATTTCTGTAAATTAAGCAACAGCTGGCTTACCAAGAGGAGGAGGAGGAGG	1080			
OY	1081	GGGCTGGAAGTAAAGAAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140			
Db	1081	GGGCTGGAAGTAAAGAAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140			
OY	1141	ATCTGAATGCTGATCCCTGTGAGAGAAAGAAATGAAATGAGGAGGAGGAGGAGGAGG	1200			
Db	1141	ATCTGAATGCTGATCCCTGTGAGAGAAAGAAATGAAATGAGGAGGAGGAGGAGGAGG	1200			
OY	1201	CAGAGAACTCTAGAGATGATGAGATGTTCTTGGATTAACACTAAATAGCAGATTCAGA	1260			
Db	1201	CAGAGAACTCTAGAGATGATGAGATGTTCTTGGATTAACACTAAATAGCAGATTCAGA	1260			
OY	1261	AACTTAATGAGTGTCTTCCAGAGTGAACCTGTAGGTTCTGATGACATCATGATG	1320			
Db	1261	AACTTAATGAGTGTCTTCCAGAGTGAACCTGTAGGTTCTGATGACATCATGATG	1320			
OY	1321	GGGAGTCTGAATCAAAATGCGCAAGTATGATGATGATGATGATGATGATGATGATG	1380			
Db	1321	GGGAGTCTGAATCAAAATGCGCAAGTATGATGATGATGATGATGATGATGATGATG	1380			
OY	1381	AATATTCGTGTTCTTCCAGAGAAATAGACTTACTGCGCAGTATCTCATGAGGCTTAA	1440			
Db	1381	AATATTCGTGTTCTTCCAGAGAAATAGACTTACTGCGCAGTATCTCATGAGGCTTAA	1440			
OY	1441	TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTATGATGATGATGATGATGATGATG	1500			
Db	1441	TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTATGATGATGATGATGATGATGATG	1500			
OY	1501	TGGAAGAACTATCGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1560			
Db	1501	TGGAAGAACTATCGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1560			
OY	1561	TAAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGGCTCCCTCAAAATA	1620			
Db	1561	TAAATTAAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGGCTCCCTCAAAATA	1620			
OY	1621	AATTAAGGTTAAAGGAGACCTACATAGGCTTCACTCGAGATTTTAAAGAAAG	1680			
Db	1621	AATTAAGGTTAAAGGAGACCTACATAGGCTTCACTCGAGATTTTAAAGAAAG	1680			
OY	1681	CAGATTTGCACTTCAAAAGACTCCTGAATGATTAATCAGGAACTTAACCAAGGAGC	1740			
Db	1681	CAGATTTGCACTTCAAAAGACTCCTGAATGATTAATCAGGAACTTAACCAAGGAGC	1740			
OY	1741	AGAATGCTCAAGTGAATTAATTAATGATGATGATGATGATGATGATGATGATGATG	1800			
Db	1741	AGAATGCTCAAGTGAATTAATTAATGATGATGATGATGATGATGATGATGATGATG	1800			
OY	1801	CTATTCAGATGAGAAAAATCTTAACCAATGATCACTCGAAAAAATAATCTGTTCA	1860			
Db	1801	CTATTCAGATGAGAAAAATCTTAACCAATGATCACTCGAAAAAATAATCTGTTCA	1860			
OY	1861	AAACGAAAGCTGAACCTATTAAGCAGATTAATGAATGAGAACTCAATTAATATCC	1920			
Db	1861	AAACGAAAGCTGAACCTATTAAGCAGATTAATGAATGAGAACTCAATTAATATCC	1920			
OY	1921	ACAAATCAAAACACCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1980			
Db	1921	ACAAATCAAAACACCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1980			
OY	1981	ATGCGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040			
Db	1981	ATGCGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040			
OY	2041	TGATAGTGTCTAGAGTGAAGATTAAGAAAAAATAACCAATGCGAGTCA	2100			
Db	2041	TGATAGTGTCTAGAGTGAAGATTAAGAAAAAATAACCAATGCGAGTCA	2100			



QY	2101	GGGACGACAAAACCTACAACTCATGTGAAGGATGAAGAACTCTCACTGAGCGAAAGA	2160
Db	2101	GGCGACGACAAAACCTACAACTCATGTGAAGGATGAAGAACTCTCACTGAGCGAAAGA	2160
QY	2161	GTAACAAGCCAAATGAAACAGACAGTAAGTAAAAAGACATGACAGCATCTCTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAAACAGACAGTAAGTAAAAAGACATGACAGCATCTCTCCAGAGCTGA	2220
QY	2281	TTGTCATCTCTACCTCTCCAAAGAGAAAAGAAAAGAGAAATCTAAAAAGTTAAAGGT	2340
Db	2281	TTGTCATCTCTACCTCTCCAAAGAGAAAAGAAAAGAGAAATCTAAAAAGTTAAAGGT	2340
QY	2341	CTAATAATGCTGAAGACCCCAAAAGATCTGATGTTAAGTGGAGAAAGGGTTTGCAAATG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAAAGATCTGATGTTAAGTGGAGAAAGGGTTTGCAAATG	2400
QY	2401	AAAGATCTGTAGAGATGAGATGATTTCAATGGTACCTGGTCTGATTAATGAGCACTAGG	2460
Db	2401	AAAGATCTGTAGAGATGAGATGATTTCAATGGTACCTGGTCTGATTAATGAGCACTAGG	2460
QY	2461	AAAGATCTGTAGAGATGAGATGATTTCAATGGTACCTGGTCTGATTAATGAGCACTAGG	2520
Db	2461	AAAGATCTGTAGAGATGAGATGATTTCAATGGTACCTGGTCTGATTAATGAGCACTAGG	2520
QY	2521	GTGTGAGTCACTGTGTGACACATTTGAAAACCCCAAGGACATAATTCATGTTGTTCCAAAG	2580
Db	2521	GTGTGAGTCACTGTGTGACACATTTGAAAACCCCAAGGACATAATTCATGTTGTTCCAAAG	2580
QY	2581	ATAATAGAAATGACACAGAAAGGCTTTTAATGATTCATTTGGGACATGAACTTAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGGCTTTTAATGATTCATTTGGGACATGAACTTAACACAGTC	2640
QY	2641	GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGGACAAATACAT	2700
Db	2641	GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGGACAAATACAT	2700
QY	2701	TCAAAGTTTCAAAGGCCCAAGTCAATTTGCTCTGTTTCAAATCCAGAGAAATGCAGAAAGG	2760
Db	2701	TCAAAGTTTCAAAGGCCCAAGTCAATTTGCTCTGTTTCAAATCCAGAGAAATGCAGAAAGG	2760
QY	2761	AATGTGCACATTTCTGTGCCACACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCACATTTCTGTGCCACACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGAAATGTGAACAAAAGGAAGAAATCAGAGAAAGATGATCTAATTCAGGCTGTAC	2880
Db	2821	TTGAAATGTGAACAAAAGGAAGAAATCAGAGAAAGATGATCTAATTCAGGCTGTAC	2880
QY	2881	AGACAGTAAATATACATGACAGGCTTCCGTGATGGTGGTCAGAAAGATTAAGCAGTGTATA	2940
Db	2881	AGACAGTAAATATACATGACAGGCTTCCGTGATGGTGGTCAGAAAGATTAAGCAGTGTATA	2940
QY	2941	ATGCCAAATGTAGTATCAAAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCCAGAGCA	3000
QY	3001	ACGAAACTGACATCTATCTCCAAATTAACATGAGACTTTTACAAAACCCATATGCTATAC	3060
Db	3001	ACGAAACTGACATCTATCTCCAAATTAACATGAGACTTTTACAAAACCCATATGCTATAC	3060
QY	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAACATTAATGTAGAAAAATCTGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAACATTAATGTAGAAAAATCTGCTAGAGG	3120
QY	3121	AAAACCTTTGAGGAACATCTCAATGTCACTCTGAGAAAGAAATGGAAATGAGAACTTCCAA	3180
Db	3121	AAAACCTTTGAGGAACATCTCAATGTCACTCTGAGAAAGAAATGGAAATGAGAACTTCCAA	3180

QY	3181	GTACAGGAGACAAATTAGCCGTAATACATTAGAGAAAATGTTTTTAAAGAGCCACT	3240
Db	3181	GTACAGTGAGACAAATTAGCCGTAATACATTAGAGAAAATGTTTTTAAAGAGCCACT	3240
QY	3241	CAACCAATATTATTAAGAAAGGTTCCAGTACTAATGAATGGGCTCCAGTATTATTAAGAA	3300
Db	3241	CAACCAATATTATTAAGAAAGGTTCCAGTACTAATGAATGGGCTCCAGTATTATTAAGAA	3300
QY	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTAGTATGAAAACAGAGGCCAAATTGA	3360
Db	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTAGTATGAAAACAGAGGCCAAATTGA	3360
QY	3361	ATGCTATGCTTAATTAAGGGGTTTTGCACACCTGAGGTCATATAACAAGTCCTCTGGAA	3420
Db	3361	ATGCTATGCTTAATTAAGGGGTTTTGCACACCTGAGGTCATATAACAAGTCCTCTGGAA	3420
QY	3421	GTAATTTAAGCAATCCGAAATATAAAGCAAGAAATATAAGATAGTCCAGCTGTA	3480
Db	3421	GTAATTTAAGCAATCCGAAATATAAAGCAAGAAATATAAGATAGTCCAGCTGTA	3480
QY	3481	ATACAGATTCTCTCCATATCTGATTTAGATTAAGTATTAAGACAGCCTATGGGAATGTC	3540
Db	3481	ATACAGATTCTCTCCATATCTGATTTAGATTAAGTATTAAGACAGCCTATGGGAATGTC	3540
QY	3541	ATGATCTCAGGTTTGTTGCTGABACACCGTATGACTGTTAATATATGTTGAATTAAGG	3600
Db	3541	ATGATCTCAGGTTTGTTGCTGABACACCGTATGACTGTTAATATATGTTGAATTAAGG	3600
QY	3601	AAAGTACTAGTTTGGCGAAATAGACATTAAAGAAAGTTCTGCTGTTTTTACCAAAACG	3660
Db	3601	AAAGTACTAGTTTGGCGAAATAGACATTAAAGAAAGTTCTGCTGTTTTTACCAAAACG	3660
QY	3661	TCCAGAAAGAGAGACTTAGCAGAGAGTCTTAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGAGAGACTTAGCAGAGAGTCTTAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
QY	3721	GTTACCCAAAGAGGGGCCAAGAAATTTAGAGTCCCTCAGAAAGAACTTACTAGTGGAGTG	3780
Db	3721	GTTACCCAAAGAGGGGCCAAGAAATTTAGAGTCCCTCAGAAAGAACTTACTAGTGGAGTG	3780
QY	3781	AAGAGCTCCCTGCTTCCAAACATTGTATTTTGGTAAAGTAACAATATACCTCTCAGT	3840
Db	3781	AAGAGCTCCCTGCTTCCAAACATTGTATTTTGGTAAAGTAACAATATACCTCTCAGT	3840
QY	3841	CTACTAGCAGTACACCGTTGCTACCGAGTGTCTGCTAAAGAACACAGAGAGATTTAT	3900
Db	3841	CTACTAGCAGTACACCGTTGCTACCGAGTGTCTGCTAAAGAACACAGAGAGATTTAT	3900
QY	3901	TATCATTTGAAGAAATAGCTTAATATGACTGCAGTACACAGGTAATATGGCAAGGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAATATGACTGCAGTACACAGGTAATATGGCAAGGCATCTC	3960
QY	3961	AGGAACATCACTTATGAGGAAACAAAAATGTCTGTAAGTCTGTTTCTTCAACAGTSCA	4020
Db	3961	AGGAACATCACTTATGAGGAAACAAAAATGTCTGTAAGTCTGTTTCTTCAACAGTSCA	4020
QY	4021	GTCGAATTTGAGAACTTGACTGCAAAATATACAAACCCAGAGATCTTTCTGATTTGGTTT	4080
Db	4021	GTCGAATTTGAGAACTTGACTGCAAAATATACAAACCCAGAGATCTTTCTGATTTGGTTT	4080
QY	4081	CGAATTTGAGAACTTGACTGCAAAATATACAAACCCAGAGATCTTTCTGATTTGGTTT	4140
Db	4081	CGAATTTGAGAACTTGACTGCAAAATATACAAACCCAGAGATCTTTCTGATTTGGTTT	4140
QY	4141	TTTTCAGATGATGAAAGAAAGGAAACGGGCTTTGGAAGAAATATATACAAAGCAAAACA	4200
Db	4141	TTTTCAGATGATGAAAGAAAGGAAACGGGCTTTGGAAGAAATATATACAAAGCAAAACA	4200
QY	4201	TGGAATTTAAACTTATAGTGAAGCAGCATCTGGGTTGTGAGAGTGAACAAAGCGCTCTGAG	4260
Db	4201	TGGAATTTAAACTTATAGTGAAGCAGCATCTGGGTTGTGAGAGTGAACAAAGCGCTCTGAG	4260
QY	4261	ACTGCTCAGAGGCTATCTCTCAGAGTACATTTTAAACACTCAGCAGAGGATACATATGC	4320

|||||  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTACATTTTAAACCACACAGAGGGATCCATGC 4330  
QY 4321 AACATTAACCTGATAAAGCTCCAGCAGGAAATGGCTGAATCTAGAGCTGTGTAAACAGC 4380  
|||||  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAATCTAGAGCTGTGTAAACAGC 4380  
QY 4381 ATGGAGACCAGCCTTCTACAGCTACCCCTTCATCATTAAGTACTCTTCCCTTGAGG 4440  
|||||  
Db 4381 ATGGAGACCAGCCTTCTACAGCTACCCCTTCATCATTAAGTACTCTTCCCTTGAGG 4440  
QY 4441 ACCTGGAAATCCAGAAACAAAGCAGATCAGAAAAAGCAGTTTACTTCAAGAAAGTA 4500  
|||||  
Db 4441 ACCTGGAAATCCAGAAACAAAGCAGATCAGAAAAAGCAGTTTACTTCAAGAAAGTA 4500  
QY 4501 GTGAATACCTTATTAAGCAGATCCAGAAAGCCTTCTGTGCTGACAAAGTTTGAGTGTCTG 4560  
|||||  
Db 4501 GTGAATACCTTATTAAGCAGATCCAGAAAGCCTTCTGTGCTGACAAAGTTTGAGTGTCTG 4560  
QY 4561 CAGATAGTTTACCACTGATTAAGAAATTAAGAACAGAGTGAAGAGTCAATCCCTTCTAAT 4620  
|||||  
Db 4561 CAGATAGTTTACCACTGATTAAGAAATTAAGAACAGAGTGAAGAGTCAATCCCTTCTAAT 4620  
QY 4621 GCCCATCATTAAGATAGTAGTGGTACATGACAGTGTCTGCGGAGCTTCAGAAATGAA 4680  
|||||  
Db 4621 GCCCATCATTAAGATAGTAGTGGTACATGACAGTGTCTGCGGAGCTTCAGAAATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGCCTCATTAAGTGTGTGATGTGAGAGACCAACAGCTGGAAG 4740  
|||||  
Db 4681 ACTACCATCTCAAGAGAGCCTCATTAAGTGTGTGATGTGAGAGACCAACAGCTGGAAG 4740  
QY 4741 AGCTGTGGCCACACGATTTACGGAACATCTTAATCTTGCCAAAGCAGAAAGTGAAGGAA 4800  
|||||  
Db 4741 AGCTGTGGCCACACGATTTACGGAACATCTTAATCTTGCCAAAGCAGAAAGTGAAGGAA 4800  
QY 4801 CCCCTTACCTGAGATCTGGAATCAGCCTTCTGTGATGACCCGTAATCTGATCTCTG 4860  
|||||  
Db 4801 CCCCTTACCTGAGATCTGGAATCAGCCTTCTGTGATGACCCGTAATCTGATCTCTG 4860  
QY 4861 AAGACAGAGCCCCAGAGTCACTGTGTGTGCAACATACATCTTCAACCTCTGATTTGA 4920  
|||||  
Db 4861 AAGACAGAGCCCCAGAGTCACTGTGTGTGCAACATACATCTTCAACCTCTGATTTGA 4920  
QY 4921 AAGTTCGCCAATTTGAAAGTTGCAAGAACTGCCAGAGTCCAGCTGCTCATCTACTG 4980  
|||||  
Db 4921 AAGTTCGCCAATTTGAAAGTTGCAAGAACTGCCAGAGTCCAGCTGCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAGAAATTTGACAG 5040  
|||||  
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAGAAATTTGACAG 5040  
QY 5041 CTTCAACAGAAAGGTTCAACAAAGAAATGTCATGTGTGTGCTGAGCTGACCCAGAG 5100  
|||||  
Db 5041 CTTCAACAGAAAGGTTCAACAAAGAAATGTCATGTGTGTGCTGAGCTGACCCAGAG 5100  
QY 5101 AATTATGCTGCTGTGCAAGTTTGCAGAAACACCATCACTTTAACTAATCTAATTA 5160  
|||||  
Db 5101 AATTATGCTGCTGTGCAAGTTTGCAGAAACACCATCACTTTAACTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTATGAAACAGATGCTGAGTTGTGTGAACGGACAC 5220  
|||||  
Db 5161 CTGAAGAGACTACTCATGTTGTATGAAACAGATGCTGAGTTGTGTGAACGGACAC 5220  
QY 5221 TGAATAATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTACTAATTTCTGGGTGACCC 5280  
|||||  
Db 5221 TGAATAATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTACTAATTTCTGGGTGACCC 5280  
QY 5281 AGCTATTTAAAGAAAGAAATCTGATGAGATGATTTTGAAGTCAAGAGAGATGTGG 5340  
|||||  
Db 5281 AGCTATTTAAAGAAAGAAATCTGATGAGATGATTTTGAAGTCAAGAGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCAAGGTCCAAAGGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
|||||

Db 5341 TCAATGGAAGAAACCAAGGTCCAAAGGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTGCTATAGGGCCCTTACCAACATGCCCCAGATCAACTGG 5460  
|||||  
Db 5401 TCAGGGGGCTAGAAATCTGTGCTATAGGGCCCTTACCAACAGGGCCCCAGATCAACTGG 5460  
QY 5461 AATGATGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGAGCTTTCATATTCACCTTG 5520  
|||||  
Db 5461 AATGATGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGAGCTTTCATATTCACCTTG 5520  
QY 5521 GCACAGGTGCCAACCAATGTGTGTGTGACAGATGCTGAGACAGAGGAAATGGCT 5580  
|||||  
Db 5521 GCACAGGTGTCCACCAATTTGTGTGTGTGTGACAGATGCTGAGACAGAGGAAATGGCT 5580  
QY 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGGACA 5640  
|||||  
Db 5581 TCCATGCAATTTGGGCAAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGGACA 5640  
QY 5641 GTGTAGCACTCTACCAAGTGTGTGAGGCACTGTGTGTGACCACTGATACCCAGATCCCCACA 5700  
|||||  
Db 5641 GTGTAGCACTCTACCAAGTGTGTGAGGCACTGTGTGTGACCACTGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
|||||  
Db 5701 GCCACTACTGA 5711

Search completed: May 27, 1999, 20:13:25  
Job time: 11965 sec

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 1999, 13:24:55 ; Search time 2617.04 Seconds  
(without alignments)  
3328.837 Million cell updates/sec

Title: US-08-798-691A-3

Perfect score: 5711  
Sequence: 1 AGCTCGCTGAGACTTCTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table:

Search: 2002476 seqs, 762712212 residues

Database :

EST:\*

1:	em_est1:*
2:	em_est2:*
3:	em_est3:*
4:	em_est4:*
5:	em_est5:*
6:	em_est6:*
7:	em_est7:*
8:	em_est8:*
9:	em_est9:*
10:	gb_est1:*
11:	gb_est2:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	gb_est6:*
16:	gb_est7:*
17:	gb_est8:*
18:	gb_est9:*
19:	gb_est10:*
20:	gb_est11:*
21:	gb_est12:*
22:	gb_est13:*
23:	gb_est14:*
24:	gb_est15:*
25:	gb_est16:*
26:	gb_est17:*
27:	gb_est18:*
28:	gb_est19:*
29:	gb_est20:*
30:	gb_est21:*
31:	gb_est22:*
32:	em_est1:*
33:	em_est2:*
34:	em_est3:*
35:	em_est4:*
36:	em_est5:*
37:	em_est6:*
38:	em_est7:*
39:	em_est8:*
40:	em_est9:*
41:	em_est10:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C	1	492.8	8.6	518	26	AA804632	OB98404.s
C	2	491.8	8.6	523	25	AA702344	AA702344 z187e03.s

C	3	472.2	8.3	487	26	AA812019	AA812019 OB39902.s
C	4	444	7.8	444	21	AA486004	AA486004 AB38603.r
C	5	437.4	7.7	488	27	AA814998	AA814998 OC07905.s
C	6	421.8	7.4	429	21	AA484941	AA484941 aa41a08.r
C	7	420.6	7.4	459	30	AI040685	AI040685 ox18D06.s
C	8	390.2	6.8	627	16	AA167963	AA167963 ms25006.r
C	9	330.4	5.8	466	28	AI016870	AI016870 ON31801.x
C	10	308	5.4	418	15	AA205474	AA205474 zq66D05.r
C	11	292.6	5.1	541	30	AI121871	AI121871 uc13c03.r
C	12	264.6	4.6	653	30	AI157105	AI157105 uc16c04.r
C	13	192.8	3.4	212	13	HSU25782	U25782 Human Chrom
C	14	138.2	2.4	717	28	AA985850	AA985850 ua67408.r
C	15	49.8	0.9	507	14	W82081	W82081 me95h06.r1
C	16	46.6	0.8	479	14	W08634	W08634 mb42b12.r1
C	17	45.8	0.8	611	21	AA549883	AA549883 0956m3 gm
C	18	43.8	0.8	261	31	AU033965	AU033965 Dictyoste
C	19	43.6	0.8	474	20	C25723	C25723 Dictyoste
C	20	43.4	0.8	485	25	C84015	C84015 Dictyoste
C	21	43.4	0.8	332	28	C92788	C92788 Dictyoste
C	22	43	0.8	389	13	C25764	C25764 Dictyoste
C	23	42.6	0.8	609	13	W27491	W27491 3198 Human
C	24	42.2	0.7	256	28	C90633	C90633 Dictyoste
C	25	41.6	0.7	808	30	AU035729	AU035729 Mus muscu
C	26	41.4	0.7	536	31	AU034856	AU034856 Dictyoste
C	27	41.2	0.7	546	19	C23656	C23656 Dictyoste
C	28	41.2	0.7	410	25	AA079630	AA079630 zm93905.s
C	29	41.2	0.7	3707	28	C83838	C83838 Dictyoste
C	30	41.2	0.7	475	25	C92045	C92045 Dictyoste
C	31	41	0.7	282	28	C91472	C91472 Dictyoste
C	32	40.8	0.7	631	21	AA550340	AA550340 148m3 gm
C	33	40.8	0.7	441	31	AI149592	AI149592 qc60d10.x
C	34	40.6	0.7	191	28	C94242	C94242 Dictyoste
C	35	40.4	0.7	439	16	AA139070	AA139070 mr1c11.r
C	36	40.4	0.7	639	28	AA850517	AA850517 EST193284
C	37	40.4	0.7	400	28	AA997396	AA997396 UT-R-C0-h
C	38	40.4	0.7	432	28	AA999035	AA999035 UT-R-C0-1
C	39	40.4	0.7	510	28	AI011669	AI011669 EST206120
C	40	40.4	0.7	399	29	AI071428	AI071428 UT-R-C2-n
C	41	40.4	0.7	536	30	AI101156	AI101156 EST210445
C	42	40.4	0.7	614	30	AI103485	AI103485 EST212774
C	43	40.4	0.7	405	30	AI113245	AI113245 UT-R-C2P-
C	44	40.4	0.7	271	30	AI137529	AI137529 UT-R-C2P-
C	45	40.4	0.7	448	31	AI235083	AI235083 EST231645

#### ALIGNMENTS

RESULT 1  
AA804632/c 518 bp mRNA  
LOCUS OB98404.s1 NCI-CGAP GCBI Homo sapiens CDNA clone IMAGE:139399  
DEFINITION similar to gb:U14680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN  
(HUMAN), mRNA sequence.

ACCESSION  
AA804632  
NID g2876033  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens

REFERENCE  
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 518)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.linn.gov/db/rp/image/image.html](http://www.bio.linn.gov/db/rp/image/image.html)

Insert Length: 2057 Std Error: 0.00  
 Seq primer: -40ml3 fwd. E from Amersham  
 High quality sequence stop: 460.

## FEATURES

source

1. 518  
 /organism="Homo sapiens"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20<sup>+</sup> IgD<sup>-</sup>),  
 provided by Dr. Louis M. Staudt (NCI). Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dt) primer  
 [5'-TGTTCCCAATCTGAAGTGGAGCGCGCCCTCTTTTCTTTTCTTTT-  
 3']. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified p773 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."  
 /db\_xref="taxon:9606"  
 /clone\_1ib="NCI\_CGAP\_GCB1"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"

BASE COUNT 120 a 97 c 91 g 210 t

ORIGIN

Query Match 8.6%; Score 492.8; DB 26; Length 518;  
 Best Local Similarity 99.2%; Pred. No. 2.8e-113;

Matches 516; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1556 AATCTAATTATAGAGCATTTGTACTGAGCCACAGATATACAGAGCGTCCCTCTAC 1615  
 |||||||  
 Db 518 AATCTAATTATAGAGCATTTGTACTGAGCCACAGATATACAGAGCGTCCCTCTAC 460  
 QY 1616 AATAAATTAAGCGTAAAAAGAGAGACTACATCAGGCGCTTCATCTGAGATTTTATCAA 1675  
 |||||||  
 Db 459 AATAAATTAAGCGTAAAAAGAGAGACTACATCAGGCGCTTCATCTGAGATTTTATCAA 401  
 QY 1676 GAAAGCAGATTGGCAGTTCAAAAGACTCCTGAATGATTAATCAGGAGTAACCAAC 1735  
 |||||||  
 Db 400 GAAAGCAGATTGGCAGTTCAAAAGACTCCTGAATGATTAATCAGGAGTAACCAAC 341  
 QY 1736 GGAGCAGAAATGCTCAAGTGAATATTACTAATAGTGTGATCAGAAATAAACAAGG 1795  
 |||||||  
 Db 340 GGAGCAGAAATGCTCAAGTGAATATTACTAATAGTGTGATCAGAAATAAACAAGG 281  
 QY 1796 TGATTCATATTCGAAGAAGAAAAATCTTAACCAATRGATCTACTGAAAAAGATCTGC 1855  
 |||||||  
 Db 280 TGATTCATATTCGAAGAAGAAAAATCTTAACCAATRGATCTACTGAAAAAGATCTGC 221  
 QY 1856 TTTCAAAAGCAAGCTGAACCTTAAGCAGCAGTATTAAGCAATGGAATCGAATTTAA 1915  
 |||||||  
 Db 220 TTTCAAAAGCAAGCTGAACCTTAAGCAGCAGTATTAAGCAATGGAATCGAATTTAA 161  
 QY 1916 TATCCACAATTCAAAAGACCTTAAGAAATAGCTGAGAGAGAGAGCTTCTTACAGGCA 1975  
 |||||||  
 Db 160 TATCCACAATTCAAAAGACCTTAAGAAATAGCTGAGAGAGAGAGCTTCTTACAGGCA 101  
 QY 1976 TATTCATGGCTGTGACTAGTGTAGTGAATCTTAAGCCCACTTAATTTGACTGAATT 2035  
 |||||||  
 Db 100 TATTCATGGCTGTGACTAGTGTAGTGAATCTTAAGCCCACTTAATTTGACTGAATT 41  
 QY 2036 GCAAAATGTAGTGTGTTCTAGAGAGTGAAGAGATTAAGAA 2075  
 |||||||

Db 40 GCAAAATGTAGTGTGTTCTAGACAGTGAAGAGAAAAAAA 1

## RESULT 2

AA702344/c

## LOCUS

DEFINITION

ACCESSION

AA702344

KEYWORDS

SOURCE

ORGANISM

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGC Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.

Seq primer: -40ml3 fwd. E from Amersham

High quality sequence stop: 165.

## FEATURES

source

1. 523  
 /organism="Homo sapiens"  
 /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)  
 with a modified polylinker; Site.1: Pac I; Site.2: Eco RI;  
 This is a subtracted version of the original Soares fetal  
 liver spleen INFILS library. 1st strand cDNA was primed  
 with a Pac I - oligo(dt) primer [5'  
 AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3']  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified p773 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."  
 /db\_xref="GDB:1352029"  
 /db\_xref="taxon:9606"  
 /clone\_1ib="Soares fetal liver spleen INFILS S1"  
 /dev\_stage="20 week post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"

BASE COUNT 127 a 97 c 99 g 200 t

ORIGIN

Query Match 8.6%; Score 491.8; DB 25; Length 523;  
 Best Local Similarity 97.5%; Pred. No. 4.9e-113;

Matches 510; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1527 AGCTCCCAACTTAAGCCATGATGAAATCAATTAATGAGCATTTGTACTGAG 1586  
 |||||||  
 Db 523 AGCTCCGTCGACTTAAGCCATGATGCAATCTTAATTTTGGAGCATTTGTACTGAG 464  
 QY 1587 CCACAGATTAATCAAGAGGCGTCCCTCAAAATAATTAAGCGTAAAGAGAGACTACA 1646  
 |||||||  
 Db 463 CCACAGATTAATCAAGAGGCGTCCCTTTCAATAATTAATCAGCGCTTAAGAGTGAACCTACA 404  
 QY 1647 TCAGGCTTCATCTGAGGATTTTATCAAGAAAGCAGATTTGGAGTTCAAAAGACTCCT 1706  
 |||||||

Db 403 TCAGGCTTCATCTGAGATTTTATCAAGAAAGAGATTTGGCAGTTCAAAAAGACTCT 344

QY 1707 GAATGATGATA-TAGGGAAGTACCAAGAGAGAGATGGTCAAGTGAATATTTAC 1765

Db 343 GAAATGATAATTCAGGAGACTAACCAAGAGAGAGATGGTCAAGTGAATATTTAC 284

QY 1766 TAATGTGTGATGAGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 1825

Db 283 TAATGTGTGATGAGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 224

QY 1826 CCCATAGATGATGATGAGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 1885

Db 223 CCCATAGATGATGATGAGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 164

QY 1886 CAGTATGAGATGATGAGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 1945

Db 163 CAGTATGAGATGATGAGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 104

QY 1946 TAGGTGAGAGAGATGATGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 2005

Db 103 TAGGTGAGAGAGATGATGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 44

QY 2006 AATCTAGAGAGATGATGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 2048

Db 43 AATCTAGAGAGATGATGATTAACAAAGAGATGATCTATTCAGATGAGAAAAATCTTA 1

RESULT 3  
AA812019/c 487 bp mRNA EST 19-FEB-1998  
LOCUS 093962.s1 NCI-CGAP GCBI Homo sapiens CDNA clone IMAGE:1333778  
DEFINITION Similar to gb:U14680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN (HMAN);, mRNA sequence.  
ACCESSION AA812019  
NID 92881630  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 487)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/bdrip/image/image.html  
Insert length: 904 Std Error: 0.00  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 464.  
Location/Qualifiers  
1. 487  
/organism="Homo sapiens"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAGTGGAGCGCGCTCTATTTTTTTTTTTTTT-

3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."  
/db\_xref="taxon:9606"  
/clone="IMAGE:1333778"  
/clone\_id="NCI-CGAP\_GCBI"  
/issue\_type="germinal center B cell"  
/lab\_host="DH108"  
/lab\_host="DH108"

BASE COUNT 109 a 91 c 85 g 202 t

ORIGIN

Query Match 8.3%; Score 472.2; DB 26; Length 487;  
Best Local Similarity 99.4%; Pred. No. 4e-108;  
Matches 474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1601 AGAGCTCCCTCACAATTAATTAAGCGTAAAGAGAGACCTATCAGGCTTCATCC 1660

Db 477 AGAGCTCCCTCACAATTAATTAAGCGTAAAGAGAGACCTATCAGGCTTCATCC 418

QY 1661 TGAGATTTTATCAAGAAAGAGATTTGGCAGTCAAAAAGACTCCTGAATGATAATCA 1720

Db 417 TGAGATTTTATCAAGAAAGAGATTTGGCAGTCAAAAAGACTCCTGAATGATAATCA 358

QY 1721 GGAAGCTAACCAAGCGAGAGATTTGTCAGATGATGATTAATTAATGATGATCA 1780

Db 357 GGAAGCTAACCAAGCGAGAGATTTGTCAGATGATGATTAATTAATGATGATCA 298

QY 1781 GAATTAACCAAGAGATGATTTATTCAGAAATGAGAAAAATCTTAACCAATGATCACT 1840

Db 297 GAATTAACCAAGAGATGATTTATTCAGAAATGAGAAAAATCTTAACCAATGATCACT 238

QY 1841 CGAAAAAGATCTGCTTCAAAAAGAGAGTGAACCTATAAGCAGCATATAATATAT 1900

Db 237 CGAAAAAGATCTGCTTCAAAAAGAGAGTGAACCTATAAGCAGCATATAATATAT 178

QY 1901 GGAAGCTGAATTAATTAATTCACAATTCAAAAGCAGCTTAAGAGATGAGAGAGAA 1960

Db 177 GGAAGCTGAATTAATTAATTCACAATTCAAAAGCAGCTTAAGAGATGAGAGAGAA 118

QY 1961 GTCTTACACGAGATATTCATGCGCTTGAACCTAGTACTGATGAATCTTAACCCACC 2020

Db 117 GTCTTACACGAGATATTCATGCGCTTGAACCTAGTACTGATGAATCTTAACCCACC 58

QY 2021 TAATGTGATGATGATGATTAATGATGATTTCTAGAGAGTGAAGATTAAGAAAAA 2077

Db 57 TAATGTGATGATGATGATTAATGATGATTTCTAGAGAGTGAAGATTAAGAAAAA 1

RESULT 4  
AA486004 444 bp mRNA EST 11-AUG-1997  
LOCUS AB386003.t1 Stragene HeLa cell s3 937216 Homo sapiens CDNA clone  
DEFINITION 843077 5 similar to gb:U14680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN (HMAN);, mRNA sequence.  
ACCESSION AA486004  
NID 92216220  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 444)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.  
TITLE Wash-Merck EST Project 1997  
JOURNAL Unpublished (1997)  
COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (infoimage.lnl.gov) for further information.  
Seq primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 431.  
Location/Qualifiers

## FEATURES

Source

1..444  
/organism="Homo sapiens"  
/note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2:  
XhoI; Cloned unidirectionally. Primer: Oligo dt. HeLa S3  
epithelioid carcinoma cells grown to semi-confluency  
without induction. Average insert size: 1.5 kb; Uni-TAP XR  
vector. ~5' adaptor sequence: 5' GAATTCGCCGAG 3' -3'  
adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3' "  
/db\_xref="taxon:9606"  
/clone="843077"  
/clone\_lib="Stratagene HeLa cell s3 937216"  
/sex="female"  
/dev\_stage="HeLa S3 cell line"  
/lab\_host="SOLR (kanamycin resistant)"  
<1..>444

BASE COUNT 170 a 76 c 86 g 112 t  
ORIGIN

Query Match 7.8%; Score 444; DB 21; Length 444;  
Best Local Similarity 100.0%; Pred. No. 4.6e-101;

Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2997 GCCAAGCAAGTCTGACTCTTCTCCAAATTAACATGAGCTTTTACCAAAACCATATCGT 3056  
1 GCCAAGCAAGTCTGACTCTTCTCCAAATTAACATGAGCTTTTACCAAAACCATATCGT 60  
3057 ATACCAACCTTTTCCATCAAGTCTTTGTTAAACTTAATGTAGAAATAATCTGCTA 3116  
61 ATACCAACCTTTTCCATCAAGTCTTTGTTAAACTTAATGTAGAAATAATCTGCTA 120  
3117 GAGGAAGCTTTGAGGAATTCATGATGACCCGGAAGAAATGGGAATGGAACATT 3176  
121 GAGGAAGCTTTGAGGAATTCATGATGACCCGGAAGAAATGGGAATGGAACATT 180  
3177 CCAGTACAGTACGACAACTTACCTTAATTAACATTAAGAAATGTTTAAAGAGCC 3236  
181 CCAGTACAGTACGACAACTTACCTTAATTAACATTAAGAAATGTTTAAAGAGCC 240  
3237 AGCTAAGCAATTAATGAGTACGATGATGATGATGATGATGATGATGATGATGAT 3296  
241 AGCTAAGCAATTAATGAGTACGATGATGATGATGATGATGATGATGATGATGAT 300  
3297 GAAATAGGTTCCAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 3356  
301 GAAATAGGTTCCAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
3357 TTGAATGCTATGCTTAGATTAGGGTTTGAACCTGAGGTCTATTAACAAAGTCTTCT 3416  
361 TTGAATGCTATGCTTAGATTAGGGTTTGAACCTGAGGTCTATTAACAAAGTCTTCT 420  
3417 GGAAGTATTTGTAAGCATCTGAA 3440  
421 GGAAGTATTTGTAAGCATCTGAA 444

RESULT 5  
AA814998/c 488 bp mRNA EST 05-MAR-1998  
LOCUS AA814998 488 bp mRNA EST 05-MAR-1998  
DEFINITION oco07905.s1 NCI-CGAP GCBI Homo sapiens cDNA clone IMAGE:1340216 3'  
similar to gb:014680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN  
(HUMAN);, mRNA sequence.

## ACCESSION

AA814998  
NID 92884594  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens

## REFERENCE

Enkaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 488)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

## JOURNAL

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/db/rp/image/image.html](http://www.bio.lnl.gov/db/rp/image/image.html)

## FEATURES

source  
1..488  
/organism="Homo sapiens"  
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified  
polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, 19D-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was  
performed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAGAGGAGGCGGCGCTCTTTT TTT TTT TTT TTT TTT TTT  
3']. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
/db\_xref="taxon:9606"  
/clone="IMAGE:1340216"  
/clone\_lib="NCI-CGAP GCBI"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"

BASE COUNT 108 a 87 c 94 g 199 t  
ORIGIN

Query Match 7.7%; Score 437.4; DB 27; Length 488;  
Best Local Similarity 97.1%; Pred. No. 2.2e-99;  
Matches 477; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

1587 CCACGATTAATCAAGACCGCTCCCTCAAAATTAATTAAGCTTAAGAGAGACTTACA 1646  
488 CCACGATTAATCAAGACCGCTCCCTCAAAATTAATTAAGCTTAAGAGAGACTTACA 429  
1647 TCAGGCTTCATCCGAGGATTTTATCAAGAAACGACATTTGCGAGTCAAAAAGCTCCT 1706  
428 TCAGGCTTCATCCGAGGATTTTATCAAGAAACGACATTTT-GCAGTCAAAAAGCTCCT 370  
1707 GAAATGATTAATCAAGGAACTTAACCAAGGAGAGAGATGTCAGTCAAGTATTAATCT 1766  
369 GAAATGATTAATCA-GGAATTAACCAAGGAGAGAGATGTCAGTCAAGTATTAATCT 311  
1767 AATAGTGTCTATGAGATTAACCAAGGAGATGTCATTTAGATGAGAGAAATCTTAAC 1826  
310 AATAGTGTCTATGAGATTAACCAAGGAGATGTCATTTAGATGAGAGAAATCTTAAC 251



QY 1827 CCAATGAAATCTCGAAAAAGAAATCTGCTTTCAAAAAGAAAGCTGAACTATATAGCAGC 1886  
 Db 250 CCAATGAAATCTCGAAAAAGAAATCTGCTTTCAAAAAGAAAGCTGAACTATATAGCAGC 191  
 QY 1887 AGATATAGCAATATGAACTGAAATTAATATCCAAATTCAAAAGCACTTAAAGAAAT 1946  
 Db 190 AGATATAGCAATATGAACTGAAATTAATATCCAAATTCAAAAGCACTTAAAGAAAT 131  
 QY 1947 AGGCTGAGAGAGAGCTCTTACACGAGCATATTCATCGCTTGAACTAGTACAGTAGA 2006  
 Db 130 AGGCTGAGAGAGAGCTCTTACACGAGCATATTCATCGCTTGAACTAGTACAGTAGA 72  
 QY 2007 AATCTAAGCCACCTAATTTACTGAAATTCGAAATTAATATGTTGTTTACAGTGAAGAG 2066  
 Db 71 AATCTAAGCCACCTAATTTACTGAAATTCGAAATTAATATGTTGTTTACAGTGAAGAG 12  
 QY 2067 ATAAAGAAAA 2077  
 Db 11 ATAAAGAAAA 1  
 RESULT 6  
 AA484941 429 bp mRNA EST 15-AUG-1997  
 LOCUS aa41808.r1 NCI-CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:815798 5'  
 DEFINITION (HUMAN); mRNA sequence.  
 accession AA484941  
 nid 92214160  
 keywords EST.  
 source human.  
 organism Homo sapiens  
 Eukaryota; Eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;  
 Homo.  
 1 (bases 1 to 429)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/bdrip/image/image.html  
 Seq primer: -28m13 rev1 ET from Amersham  
 High quality sequence stop: 414.  
 Location/Qualifiers  
 1..429  
 /organism="Homo sapiens"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 [5'-TGTTCACCAATCTGAAGTGGAGCGGCGCTCATTTTCTTTTCTTTT-  
 3']. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

/db\_xref="taxon:9606"  
 /clone="IMAGE:815798"  
 /clone\_1b="NCI-CGAP\_GCB1"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 <1..>429  
 /db\_xref="GDB:6035419"  
 BASE COUNT 153 a 70 c 101 g 105 t  
 ORIGIN  
 Query Match 7.4%; Score 421.8; DB 21; Length 429;  
 Best Local Similarity 99.5%; Pred. No. 1; re-95;  
 Matches 423; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2311 AACAGAGAACTAGAAACAGTTAAAGTGTCTATATATGCTGAAGACCCCAAGATCTCA 2370  
 Db 5 AGGAGAGAACTAGAAACAGTTAAAGTGTCTATATATGCTGAAGACCCCAAGATCTCA 64  
 QY 2371 TGTTAAGTGAGAAAGGTTTGCAAAACGTGAAGATCTGTAGAGAGTAGCAGTATTTTCAT 2430  
 Db 65 TGTTAAGTGAGAAAGGTTTGCAAAACGTGAAGATCTGTAGAGAGTAGCAGTATTTTCAT 124  
 QY 2431 TGTACTCTGTACTGATTAATGACACCTAGGAAGTATCTGCTACTGAGATAGACATC 2490  
 Db 125 TGTACTCTGTACTGATTAATGACACCTAGGAAGTATCTGCTACTGAGATAGACATC 184  
 QY 2491 TAGGGAAGGCAAAACAGAACCAATTAATGTGTGATCAGTGTGCAGCATTTGAAACC 2550  
 Db 185 TAGGGAAGGCAAAACAGAACCAATTAATGTGTGATCAGTGTGCAGCATTTGAAACC 244  
 QY 2551 CCAAGGAGCTAATTCATGTTGTTCCAAAGATATATAGAAATGACACAGAAAGCTTTAAGT 2610  
 Db 245 CCAAGGAGCTAATTCATGTTGTTCCAAAGATATATAGAAATGACACAGAAAGCTTTAAGT 304  
 QY 2611 ATCCATTGGGACATGAAGTTAACACACAGTGGGAAACACATATAGAAATGAGAAAGT 2670  
 Db 305 ATCCATTGGGACATGAAGTTAACACACAGTGGGAAACACATATAGAAATGAGAAAGT 364  
 QY 2671 AACTGTATGCTCAGTATTTTGCAGAAATCATTCAGAGTTTCAAGCGCCAGTCTTCTC 2730  
 Db 365 AACTGTATGCTCAGTATTTTGCAGAAATCATTCAGAGTTTCAAGCGCCAGTCTTCTC 424  
 QY 2731 TGTTT 2735  
 Db 425 CGTTT 429  
 RESULT 7  
 A1040685/c 459 bp mRNA EST 28-AUG-1998  
 LOCUS A1040685 459 bp mRNA EST 28-AUG-1998  
 DEFINITION oxi18B06.s1 Soares fetal liver spleen INF5.s1 Homo sapiens cDNA  
 clone IMAGE:165659.3 similar to gb:014680 BREAST CANCER TYPE 1  
 SUSCEPTIBILITY PROTEIN (HUMAN); mRNA sequence.  
 accession A1040685  
 nid 93279879  
 keywords EST.  
 source human.  
 organism Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 459)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Trace considered overall poor quality









OY	1970	CAGGATATTCTACGGCCCTGAACCTAGTACGTAGCAAAATCTAAGCCCACTTAATTGAC	2029
Db	1		60
OY	2030	TGAATTGCCAAATTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAAGTACAACCA	2089
Db	61		120
OY	2090	AATGCACAGCAGGCACAGACAGAAGAACTATAAACCTCATGGAAGGTAAAGAAACCCTCAACTGG	2149
Db	121		180
OY	2150	AATGCACAGCAGGCACAGACAGAAGAACTATAAACCTCATGGAAGGTAAAGAAACCCTCAACTGG	180
Db	181		212
RESULT	14		
LOCUS	AA985850		
DEFINITION	AA985850	717 bp mRNA EST 28-MAY-1998	
REFERENCE	UA672808 r1 Soares 2dbmt Mus musculus cDNA clone 1362518 5' similar to gb:U14680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN (HDN); gb:U36475 Mus musculus breast and ovarian cancer susceptibility protein (MOUSE); , mRNA sequence.		
ACCESSION	AA985850		
NID	G3167239		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 717)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The WashU-HHMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:895738 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 407. Location/Qualifiers 1..717 /organism="Mus musculus" /strain="C57BL/6J" /note="Vector: pRT7D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTCACATCTGAAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT7 vector. RNA provided by Dr. Bert Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo." /db_xref="taxon:10090" /clone="1362518" /sex="male" /tissue_type="Thymus" /dev_stage="4 weeks"		
FEATURES	Source		

[illegible]





